

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: December 27, 2001, 14:49:08 ; Search time 1726.63 Seconds
(without alignments)
11207.492 Million cell updates/sec

Title: US-09-435-054-1
Perfect score: 1173
Sequence: 1 ccacgctccgccaccacac.....tcaaaaaaaaaaaaaaaa 1173

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1091308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htgo_hum.*
- 31: em.htgo_inv.*
- 32: em.htgo_rod.*
- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	30	2.6	214005	2	AC064803	Mus muscu
C 2	29	2.5	185996	2	AC041023	Homo sapi
C 3	26	2.2	602	8	LES133600	Lycopersi
C 4	26	2.2	2518	3	AF309947	Dictyoste
C 5	26	2.2	2580	3	AF145620	Drosophil
C 6	26	2.2	5575	9	HSM802758	Homo sapi
C 7	26	2.2	110000	2	PFMAL4P1_0	Plasmodiu
C 8	26	2.2	163443	2	AC006280	Plasmodiu
C 9	26	2.2	207596	2	AL590630	Mus muscu
C 10	25	2.1	1318	8	NTUPGENE	N tabacum m
C 11	25	2.1	1445	5	GSK60GENE	Gallus gall
C 12	25	2.1	1498	3	CE19144	Ceratitis c
C 13	25	2.1	1572	3	CCA19145	Ceratitis c
C 14	25	2.1	1633	9	AK026358	Homo sapi
C 15	25	2.1	1683	3	AF057693	Sacculina
C 16	25	2.1	1705	3	DDU20806	Dictyosteli
C 17	25	2.1	1891	3	OVI15993	Onchocerca
C 18	25	2.1	2691	5	XL059483	Xenopus lae
C 19	25	2.1	2703	5	XL089707	Xenopus lae
C 20	25	2.1	2771	3	AF083225	Caenorhab
C 21	25	2.1	3268	3	PFRESAG1	P. falciparu
C 22	25	2.1	4591	6	A00661	P. falciparu
C 23	25	2.1	20413	9	AC004631	Homo sapi
C 24	25	2.1	25147	2	AC014449	Drosophil
C 25	25	2.1	34000	9	AC006540	Homo sapi
C 26	25	2.1	43324	2	AC034287	Mus muscu
C 27	25	2.1	47827	8	AP000731	Arabidops
C 28	25	2.1	57698	9	HSJ753M9	Human DNA
C 29	25	2.1	63331	2	AC084345	Homo sapi
C 30	25	2.1	73880	2	AC090728	Homo sapi
C 31	25	2.1	81447	2	AC034306	Homo sapi
C 32	25	2.1	83948	8	AB012246	Arabidops
C 33	25	2.1	85812	2	AC040952	Homo sapi
C 34	25	2.1	86677	2	AC005646	Drosophil
C 35	25	2.1	86827	3	PFMAL3P5	Plasmodiu
C 36	25	2.1	87400	8	AC010796	Arabidops
C 37	25	2.1	95477	9	AC007076	Homo sapi
C 38	25	2.1	101157	9	AL356791	Human DNA
C 39	25	2.1	128266	9	AC008623	Homo sapi
C 40	25	2.1	131541	2	AC006594	Homo sapi
C 41	25	2.1	135056	9	AL445071	Human DNA
C 42	25	2.1	142239	8	AF003266	Oryza sat
C 43	25	2.1	144075	2	AC013763	Homo sapi
C 44	25	2.1	146574	2	AC023459	Homo sapi
C 45	25	2.1	147246	2	AC023196	Homo sapi
C 46	25	2.1	149008	9	AC007991	Homo sapi
C 47	25	2.1	152409	2	PFMAL1P1	Plasmodiu
C 48	25	2.1	153846	2	AC023252	Homo sapi
C 49	25	2.1	156847	33	AC073662	Homo sapi
C 50	25	2.1	157525	2	AC083838	Homo sapi
C 51	25	2.1	157747	2	AL158834	Homo sapi
C 52	25	2.1	159468	2	AC015280	Drosophil
C 53	25	2.1	160209	9	AC012324	Homo sapi
C 54	25	2.1	160903	3	AC007580	Drosophil
C 55	25	2.1	162908	2	AC046195	Homo sapi
C 56	25	2.1	163345	2	AL360002	Homo sapi
C 57	25	2.1	165106	2	AC016034	Homo sapi
C 58	25	2.1	165868	9	AC010651	Homo sapi
C 59	25	2.1	166076	2	AC090587	Homo sapi
C 60	25	2.1	169103	2	AC025687	Homo sapi
C 61	25	2.1	169210	2	AC055841	Homo sapi
C 62	25	2.1	169689	3	AC008306	Drosophil
C 63	25	2.1	170282	3	AC006467	Drosophil
C 64	25	2.1	171805	9	AC020716	Homo sapi
C 65	25	2.1	173760	9	AL354653	Human DNA
C 66	25	2.1	174084	2	AC090695	Homo sapi
C 67	25	2.1	174551	9	AC010598	Homo sapi
C 68	25	2.1	175872	33	AC011878	Homo sapi
C 69	25	2.1	175952	2	AC012060	Homo sapi
C 70	25	2.1	176278	2	AC091305	Homo sapi

71	25	2.1	177309	2	AL592226	AL592226 Homo sapi	144	24	2.0	95870	8	AC026757	AC026757 Arabidops
72	25	2.1	178035	2	AC068680	AC068680 Homo sapi	145	24	2.0	96299	9	AL133519	AL133519 Human DNA
73	25	2.1	179550	2	AL603626	AL603626 Homo sapi	146	24	2.0	97684	9	HS0309122	298256 Human DNA s
74	25	2.1	179936	2	AC025491	AC025491 Homo sapi	147	24	2.0	100000	9	AP0000084	AP0000084 Homo sapi
75	25	2.1	180551	9	HUAC004158	AC004158 Homo sapi	148	24	2.0	100000	9	AP000136	AP000136 Homo sapi
76	25	2.1	181006	2	AC020780	AC020780 Homo sapi	149	24	2.0	107554	2	AC084697	AC084697 Homo sapi
77	25	2.1	181166	2	AC025251	AC025251 Homo sapi	150	24	2.0	109173	9	AC007678	AC007678 Homo sapi
78	25	2.1	181636	2	AC025108	AC025108 Homo sapi	151	24	2.0	109612	9	AL512503	AL512503 Human DNA
79	25	2.1	183560	2	AP003063	AP003063 Homo sapi	152	24	2.0	110000	2	AC046137_3	Continuation (4 of
80	25	2.1	183892	2	AC092977	AC092977 Homo sapi	153	24	2.0	110000	2	AL354792_2	Continuation (3 of
81	25	2.1	183918	2	AC025896	AC025896 Homo sapi	154	24	2.0	110015	2	AL450323	AL450323 Mus muscu
82	25	2.1	185764	2	AC025289	AC025289 Homo sapi	155	24	2.0	111694	9	HSJ3836N17	AL049539 Human DNA
83	25	2.1	191674	2	AC022975	AC022975 Homo sapi	156	24	2.0	115995	9	AC011494	AC011494 Homo sapi
84	25	2.1	196725	2	AC055873	AC055873 Homo sapi	157	24	2.0	116524	9	AL138686	AL138686 Human DNA
85	25	2.1	197872	2	AC037476	AC037476 Homo sapi	158	24	2.0	117616	2	AC091249	AC091249 Mus muscu
86	25	2.1	199551	2	AC006281	AC006281 Plasmodi	159	24	2.0	118492	2	AC020548	AC020548 Homo sapi
87	25	2.1	201327	2	AL591709	AL591709 Homo sapi	160	24	2.0	119456	2	AC084789	AC084789 Homo sapi
88	25	2.1	201874	2	AC026472	AC026472 Homo sapi	161	24	2.0	119484	9	AC005064	AC005064 Homo sapi
89	25	2.1	205429	2	AC005506	AC005506 Plasmodi	162	24	2.0	120433	2	AC092287	AC092287 Homo sapi
90	25	2.1	212658	2	AC068868	AC068868 Homo sapi	163	24	2.0	121245	2	AC034240	AC034240 Homo sapi
91	25	2.1	260713	3	AE003814	AE003814 Drosophil	164	24	2.0	122056	9	AF283320S1	AF283320 Homo sapi
92	25	2.1	293431	2	PFMAL13P4	AL049181 Plasmodi	165	24	2.0	122302	9	AC003982	AC003982 Homo sapi
93	25	2.1	298283	3	AE003782	AE003782 Drosophil	166	24	2.0	122742	9	HS167P19	293014 Homo sapien
94	25	2.1	321003	2	PFMAL4P3	AL035476 Plasmodi	167	24	2.0	124048	9	HUAC002045	AC002045 Human Chr
95	24	2.0	542	8	AF336985	AF336985 Vaucheria	168	24	2.0	131329	2	AL354887	AL354887 Homo sapi
96	24	2.0	666	8	CAR7556	AJ007556 Cicer ari	169	24	2.0	135276	2	AC073603	AC073603 Mus muscu
97	24	2.0	837	8	AF015785	AF015785 Phaseolus	170	24	2.0	135369	2	AC090557	AC090557 Homo sapi
98	24	2.0	886	6	AR123127	AR123127 Sequence	171	24	2.0	135552	9	AL19251	AL19251 Homo sapi
99	24	2.0	886	6	AR124079	AR124079 Sequence	172	24	2.0	138347	9	AL389889	AL389889 Human DNA
100	24	2.0	886	8	AF243376	AF243376 Glycine m	173	24	2.0	143427	9	AC002432	AC002432 Human BAC
101	24	2.0	937	5	CCA308993	AJ308993 Cyprinops	174	24	2.0	143804	2	AC012617	AC012617 Homo sapi
102	24	2.0	1030	8	AF003728	AF003728 Arabidops	175	24	2.0	144449	2	AC067926	AC067926 Mus muscu
103	24	2.0	1210	9	BC009956	BC009956 Homo sapi	176	24	2.0	144694	2	AC011321	AC011321 Homo sapi
104	24	2.0	1372	9	AF144755	AF144755 Homo sapi	177	24	2.0	144877	2	AL157408	AL157408 Homo sapi
105	24	2.0	1431	9	BC000409	BC000409 Homo sapi	178	24	2.0	145988	2	AC024059	AC024059 Homo sapi
106	24	2.0	1466	6	AX105363	AX105363 Sequence	179	24	2.0	146006	9	AC005103	AC005103 Homo sapi
107	24	2.0	1520	9	BC009376	BC009376 Homo sapi	180	24	2.0	146006	9	AC005103	AC005103 Homo sapi
108	24	2.0	1552	8	AF246715	AF246715 Phalaenop	181	24	2.0	146460	33	AC007913	AC007913 Homo sapi
109	24	2.0	1606	3	DD041222	U41222 Dictyosteli	182	24	2.0	147327	2	AC078905	AC078905 Homo sapi
110	24	2.0	1890	9	AB051123	AB051123 Macaca fa	183	24	2.0	147386	2	AC092065	AC092065 Homo sapi
111	24	2.0	1928	6	AX192162	AX192162 Sequence	184	24	2.0	147621	2	AC060763	AC060763 Homo sapi
112	24	2.0	2031	9	BC000964	BC000964 Homo sapi	185	24	2.0	147708	9	HS179M20	297053 Human DNA s
113	24	2.0	2040	9	BC007746	BC007746 Homo sapi	186	24	2.0	147889	2	AC018534	AC018534 Homo sapi
114	24	2.0	2210	9	AB056838	AB056838 Macaca fa	187	24	2.0	148260	2	AL596222	AL596222 Homo sapi
115	24	2.0	2214	8	MTR310820	AJ310820 Medicago	188	24	2.0	149542	9	AC011711	AC011711 Homo sapi
116	24	2.0	2259	9	AK025591	AK025591 Homo sapi	189	24	2.0	150150	2	AC022003	AC022003 Homo sapi
117	24	2.0	2307	8	MSA311050	AJ311050 Medicago	190	24	2.0	150959	2	AC019250	AC019250 Homo sapi
118	24	2.0	2327	6	AR087435	AR087435 Sequence	191	24	2.0	150959	2	AC019250	AC019250 Homo sapi
119	24	2.0	2858	10	BC003239	BC003239 Mus muscu	192	24	2.0	151479	2	AC012278	AC012278 Homo sapi
120	24	2.0	2993	6	AR071756	AR071756 Sequence	193	24	2.0	151964	9	AF047825	AF047825 Homo sapi
121	24	2.0	3000	9	AK026673	AK026673 Homo sapi	194	24	2.0	151964	9	AF047825	AF047825 Homo sapi
122	24	2.0	3114	3	DVI249251	AJ249251 Drosophil	195	24	2.0	152450	2	AC090141	AC090141 Homo sapi
123	24	2.0	3601	9	HSN801924	AL137651 Homo sapi	196	24	2.0	152450	2	AC090141	AC090141 Homo sapi
124	24	2.0	3997	9	AK025513	AK025513 Homo sapi	197	24	2.0	152499	2	AC032008	AC032008 Homo sapi
125	24	2.0	7236	3	AF310890	AF310890 Dictyoste	198	24	2.0	154312	2	AC011492	AC011492 Homo sapi
126	24	2.0	7622	3	AF112367	AF112367 Plasmodi	199	24	2.0	154467	2	AC022566	AC022566 Homo sapi
127	24	2.0	13684	3	AE001403	AE001403 Plasmodi	200	24	2.0	155139	2	AC025690	AC025690 Homo sapi
128	24	2.0	14613	3	AE001396	AE001396 Plasmodi	201	24	2.0	155621	2	AL590436	AL590436 Homo sapi
129	24	2.0	15861	3	AE001413	AE001413 Plasmodi	202	24	2.0	156510	2	AL356976	AL356976 Homo sapi
130	24	2.0	3522	9	AC068948	AC068948 Homo sapi	203	24	2.0	156549	2	AC079072	AC079072 Homo sapi
131	24	2.0	41924	2	AC087403	AC087403 Homo sapi	204	24	2.0	156671	2	AC027431	AC027431 Homo sapi
132	24	2.0	43241	9	HSJ9613	AJ009613 Homo sapi	205	24	2.0	157436	2	AC025682	AC025682 Homo sapi
133	24	2.0	43597	2	AC010417	AC010417 Homo sapi	206	24	2.0	157579	2	AC011152	AC011152 Homo sapi
134	24	2.0	48563	2	AC092824	AC092824 Homo sapi	207	24	2.0	158431	9	AC008115	AC008115 Homo sapi
135	24	2.0	61013	2	AC090456	AC090456 Homo sapi	208	24	2.0	160114	2	AC032073	AC032073 Homo sapi
136	24	2.0	61209	9	AP000220	AP000220 Homo sapi	209	24	2.0	160979	2	AC055879	AC055879 Homo sapi
137	24	2.0	71306	9	AC007423	AC007423 Homo sapi	210	24	2.0	161164	2	AC022278	AC022278 Homo sapi
138	24	2.0	71196	2	AL590419_3	Continuation (4 of	211	24	2.0	161428	2	AC022679	AC022679 Homo sapi
139	24	2.0	73395	9	AC008848	AC008848 Homo sapi	212	24	2.0	161692	2	AC090179	AC090179 Homo sapi
140	24	2.0	75588	9	AL356742	AL356742 Human DNA	213	24	2.0	162452	2	AC069239	AC069239 Homo sapi
141	24	2.0	79779	9	HSJ710H13	AL121712 Human DNA	214	24	2.0	162573	9	CNS00M8L	AL079304 Human Chr
142	24	2.0	83844	2	AC008708	AC008708 Homo sapi	215	24	2.0	162959	2	AC019255	AC019255 Homo sapi
143	24	2.0	95173	8	AC068324	AC068324 Arabidops	216	24	2.0	163871	9	HS1158E12	AL031584 Human DNA

217	24	2.0	164471	2	AC069500	Homo sapi
218	24	2.0	164584	2	AC021469	Homo sapi
c 219	24	2.0	164975	2	AC092702	Homo sapi
c 220	24	2.0	165077	2	AC024493	Homo sapi
c 221	24	2.0	165077	2	AC024493	Homo sapi
c 222	24	2.0	165053	2	AC0979780	Homo sapi
c 223	24	2.0	166003	2	AC091559	Homo sapi
c 224	24	2.0	166332	2	AC068955	Homo sapi
c 225	24	2.0	167294	2	AC013814	Homo sapi
c 226	24	2.0	168384	2	AC068774	Homo sapi
c 227	24	2.0	168799	9	AC009531	Homo sapi
c 228	24	2.0	168872	9	AC073325	Homo sapi
c 229	24	2.0	168880	9	AC073325	Homo sapi
c 230	24	2.0	169546	2	AC004157	Plasmodiu
c 231	24	2.0	169647	2	AC025343	Homo sapi
c 232	24	2.0	169851	2	AL592211	Homo sapi
c 233	24	2.0	170118	9	AC012384	Homo sapi
c 234	24	2.0	170389	2	AC016225	Homo sapi
c 235	24	2.0	170394	2	AC024371	Homo sapi
c 236	24	2.0	170473	2	AC021523	Homo sapi
c 237	24	2.0	170814	2	AC021686	Homo sapi
c 238	24	2.0	171304	2	AC090297	Homo sapi
c 239	24	2.0	171757	9	CNS01180	Human chr
c 240	24	2.0	171965	2	AC027507	Homo sapi
c 241	24	2.0	172033	2	AC008949	Homo sapi
c 242	24	2.0	172757	2	AL591848	Homo sapi
c 243	24	2.0	173310	2	AC090454	Homo sapi
c 244	24	2.0	173801	2	AC022257	Homo sapi
c 245	24	2.0	173825	2	AC011037	Homo sapi
c 246	24	2.0	174147	9	AC011891	Homo sapi
c 247	24	2.0	174642	2	AC091769	Homo sapi
c 248	24	2.0	175684	2	AC073343	Homo sapi
c 249	24	2.0	176226	2	AC026583	Homo sapi
c 250	24	2.0	176806	2	AC090438	Homo sapi
c 251	24	2.0	176976	2	AC012213	Homo sapi
c 252	24	2.0	177263	2	AC079775	Homo sapi
c 253	24	2.0	177444	2	AC084238	Homo sapi
c 254	24	2.0	178089	2	AC093133	Papio cyn
c 255	24	2.0	178252	2	AC023933	Homo sapi
c 256	24	2.0	179428	2	AC068531	Homo sapi
c 257	24	2.0	179780	2	AC021013	Homo sapi
c 258	24	2.0	180676	2	AC022080	Homo sapi
c 259	24	2.0	180836	2	AC025241	Homo sapi
c 260	24	2.0	181413	2	AC023818	Homo sapi
c 261	24	2.0	181712	2	AF001103	Homo sapi
c 262	24	2.0	181923	9	AC022872	Homo sapi
c 263	24	2.0	181991	2	AC068322	Homo sapi
c 264	24	2.0	182641	2	AC008021	Homo sapi
c 265	24	2.0	183414	2	AC024188	Homo sapi
c 266	24	2.0	184643	2	AC087650	Homo sapi
c 267	24	2.0	184831	2	AC016030	Homo sapi
c 268	24	2.0	185939	2	AL451007	Homo sapi
c 269	24	2.0	186406	2	AC087828	Homo sapi
c 270	24	2.0	186785	9	AC010267	Homo sapi
c 271	24	2.0	187009	2	AC061710	Homo sapi
c 272	24	2.0	187292	2	AC061711	Homo sapi
c 273	24	2.0	189126	2	AC016670	Homo sapi
c 274	24	2.0	189245	2	AC018466	Homo sapi
c 275	24	2.0	189570	2	AC019120	Homo sapi
c 276	24	2.0	189791	2	AC011629	Homo sapi
c 277	24	2.0	190815	9	AC007066	Homo sapi
c 278	24	2.0	190950	2	AL359639	Homo sapi
c 279	24	2.0	191312	2	AF001030	Homo sapi
c 280	24	2.0	192929	2	AC005505	Plasmodiu
c 281	24	2.0	194391	2	AC091245	Homo sapi
c 282	24	2.0	194841	2	AC021139	Homo sapi
c 283	24	2.0	196841	2	AC018901	Homo sapi
c 284	24	2.0	196900	2	AC074366	Homo sapi
c 285	24	2.0	196930	2	AL359758	Homo sapi
c 286	24	2.0	197103	2	AC027544	Homo sapi
c 287	24	2.0	197278	2	AF001850	Homo sapi
c 288	24	2.0	197639	2	AL365504	Homo sapi
c 289	24	2.0	197844	2	AC079176	Homo sapi
c 290	24	2.0	198016	2	AC021387	Homo sapi
c 291	24	2.0	198600	2	AC005528	Mus muscu
c 292	24	2.0	200000	2	AC008076	Homo sapi
c 293	24	2.0	200168	9	AC008760	Homo sapi
c 294	24	2.0	201804	2	AC091754	Papio cyn
c 295	24	2.0	203420	2	AC074207	Mus muscu
c 296	24	2.0	204407	2	AC090443	Mus muscu
c 297	24	2.0	204703	2	AC092698	Homo sapi
c 298	24	2.0	206281	2	AL160282	Homo sapi
c 299	24	2.0	208172	2	AC093164	Homo sapi
c 300	24	2.0	210359	9	HS4430K20	Human DNA
c 301	24	2.0	211039	2	AC068555	Homo sapi
c 302	24	2.0	213973	2	AC083948	Mus muscu
c 303	24	2.0	215164	2	AL136368	Homo sapi
c 304	24	2.0	215260	2	AC073796	Mus muscu
c 305	24	2.0	218195	2	AC009600	Homo sapi
c 306	24	2.0	218829	2	AC078926	Homo sapi
c 307	24	2.0	223864	2	AL593847	Homo sapi
c 308	24	2.0	237653	2	AC073760	Mus muscu
c 309	24	2.0	300503	2	AC010260	Homo sapi
c 310	24	2.0	310779	2	AC005140	Plasmodiu
c 311	24	2.0	340000	9	AP001693	Homo sapi
c 312	23	2.0	42	6	AR020971	Sequence
c 313	23	2.0	42	6	AR043386	Sequence
c 314	23	2.0	42	6	AR062301	Sequence
c 315	23	2.0	48	6	AR020989	Sequence
c 316	23	2.0	48	6	AR043404	Sequence
c 317	23	2.0	48	6	AR062319	Sequence
c 318	23	2.0	312	9	HS184XG5	H. sapiens
c 319	23	2.0	314	5	AF266226	Gillichth
c 320	23	2.0	396	6	AF266226	Gillichth
c 321	23	2.0	401	6	AF093212	Sequence
c 322	23	2.0	478	3	AF352722	Cooperia
c 323	23	2.0	572	9	HST000258	Homo sapi
c 324	23	2.0	615	9	HSFALL39	H. sapiens m
c 325	23	2.0	634	9	HSCAP18PN	H. sapiens m
c 326	23	2.0	671	9	BC012164	Homo sapi
c 327	23	2.0	671	9	BC007606	Homo sapi
c 328	23	2.0	714	3	AB038152	Homo sapi
c 329	23	2.0	750	9	HST000256	Homo sapi
c 330	23	2.0	753	9	HSB002224	Homo sapi
c 331	23	2.0	760	6	AX003614	Sequence
c 332	23	2.0	790	9	AF339770	Homo sapi
c 333	23	2.0	812	10	AB039823	Rattus no
c 334	23	2.0	819	8	LAU89841	Lupinus ang
c 335	23	2.0	835	9	AK024767	Homo sapi
c 336	23	2.0	854	9	BC005921	Homo sapi
c 337	23	2.0	906	6	AX156357	Sequence
c 338	23	2.0	907	10	CPDPPPKI	C. porcellus
c 339	23	2.0	991	10	CPGPPPKI	C. porcellus
c 340	23	2.0	991	8	AF336285	Gossypium
c 341	23	2.0	1005	9	HOM6PSG1	Homo sapi
c 342	23	2.0	1005	9	BC002819	Homo sapi
c 343	23	2.0	1006	10	CPBPPTKI	C. porcellus
c 344	23	2.0	1014	9	BC008418	Homo sapi
c 345	23	2.0	1036	6	AR103435	Sequence
c 346	23	2.0	1056	10	AF038848	Mus muscu
c 347	23	2.0	1079	8	AY045976	Arabidops
c 348	23	2.0	1082	3	DDU06453	Dicystosteli
c 349	23	2.0	1106	8	AF093616	Acetabula
c 350	23	2.0	1140	3	SCMEGGANT	Schistosoma
c 351	23	2.0	1166	10	BC003454	Mus muscu
c 352	23	2.0	1168	10	MMICAM2	X65493 M. musculus
c 353	23	2.0	1223	8	THCHIT33	X80006 T. harzianum
c 354	23	2.0	1239	10	AF000577	Rattus no
c 355	23	2.0	1244	8	ATSEB2	Y14424 Arabidops
c 356	23	2.0	1246	9	HSV526F1B	Human DNA s
c 357	23	2.0	1261	9	HST000208	AL079294 Homo sapi
c 358	23	2.0	1279	10	BC002125	Mus muscu
c 359	23	2.0	1280	9	BC000491	Homo sapi
c 360	23	2.0	1282	9	BC000504	Homo sapi
c 361	23	2.0	1300	9	BC000794	Homo sapi
c 362	23	2.0	1301	9	HSB802748	Homo sapi

363	23	2.0	1310	3	AF202634	AF202634 Drosophill	436	23	2.0	2495	6	A83552	A83552 Sequence 1
364	23	2.0	1314	5	CCQPD1U	Y14631 Cyprin ca	437	23	2.0	2495	8	NTCHLDMC	Y10022 N. tabacum m
365	23	2.0	1359	4	AF020510	AF020510 Bos tauru	438	23	2.0	2508	10	BC006674	BC006674 Mus muscu
366	23	2.0	1382	3	AF317731	AF317731 Schistos	439	23	2.0	2568	3	DDP8A7	X51947 Dictyostell
367	23	2.0	1412	9	S78159	S78159 Homo sapien	440	23	2.0	2582	3	AK025715	AK025715 Homo sapi
368	23	2.0	1414	9	AF131847	AF131847 Homo sapi	441	23	2.0	2591	8	AF036873	AF036873 Phaneroch
369	23	2.0	1451	3	AF201906	AF201906 Drosophill	442	23	2.0	2672	9	HSCSEIG7	AF036873 Homo sapi
370	23	2.0	1452	3	AF380366	AF380366 Schistos	443	23	2.0	2678	5	AF016244	AF016244 Drosophill
371	23	2.0	1453	9	AK000191	AK000191 Homo sapi	444	23	2.0	2680	9	BC002549	BC002549 Homo sapi
372	23	2.0	1502	5	AF132447	AF132447 Drosophill	445	23	2.0	2722	9	BC007319	BC007319 Homo sapi
373	23	2.0	1506	22	E09126	E09126 cDNA encodi	446	23	2.0	2746	9	AF064087	AF064087 Homo sapi
374	23	2.0	1532	6	AX000692	AX000692 Sequence	447	23	2.0	2751	9	HSU0191	U80191 Human TFIID
375	23	2.0	1534	9	HSU001279	AL122116 Homo sapi	448	23	2.0	2754	9	AF062537	AF062537 Homo sapi
376	23	2.0	1535	8	NPY08292	Y08292 N. plumbagin	449	23	2.0	2886	9	HSU02641	AL353936 Homo sapi
377	23	2.0	1548	9	AK000609	AK000609 Homo sapi	450	23	2.0	2946	3	CEL27649	AJ277649 Caenorhab
378	23	2.0	1548	9	BC000784	BC000784 Homo sapi	451	23	2.0	2985	3	BC005140	BC005140 Homo sapi
379	23	2.0	1559	10	MMU07635	U07635 Mus musculu	452	23	2.0	3016	3	DDU31631	U31631 Dictyostell
380	23	2.0	1582	9	BC000596	BC000596 Homo sapi	453	23	2.0	3073	9	BC003138	BC003138 Homo sapi
381	23	2.0	1597	8	AF338237	AF338237 Zantedesc	454	23	2.0	3080	4	DOGFXA	AL137446 Homo sapi
382	23	2.0	1662	9	BC008718	BC008718 Homo sapi	455	23	2.0	3109	9	HSU02156	AK000054 Homo sapi
383	23	2.0	1671	3	AF140780	AF140780 Dictyoste	456	23	2.0	3229	9	AK000054	AF300334 Dictyoste
384	23	2.0	1686	8	SOL250433	AJ250433 Spinacia	457	23	2.0	3392	3	AF300334	AF300334 Dictyoste
385	23	2.0	1689	9	HSU0802149	AL137697 Homo sapi	458	23	2.0	3460	9	HSU0800879	AF283323 Caenorhab
386	23	2.0	1708	3	TRC223614	AJ223614 Tribolium	459	23	2.0	3701	3	AF283323	AF283323 Caenorhab
387	23	2.0	1731	8	AY035141	AY035141 Arabidops	460	23	2.0	3719	3	AF283322	AF283322 Caenorhab
388	23	2.0	1749	10	AF084568	AF084568 Mesocrice	461	23	2.0	3833	9	AF399910	AF399910 Homo sapi
389	23	2.0	1750	10	AF084569	AF084569 Mesocrice	462	23	2.0	4000	8	ZMA250986	AJ250986 Zea mays
390	23	2.0	1752	9	BC002642	BC002642 Homo sapi	463	23	2.0	4205	6	AX035940	AX035940 Sequence
391	23	2.0	1755	9	AF052099	AF052099 Homo sapi	464	23	2.0	4205	6	AX035940	AX035940 Sequence
392	23	2.0	1779	9	AK026307	AK026307 Homo sapi	465	23	2.0	4205	6	AF084558	AF084558 Homo sapi
393	23	2.0	1782	9	BC002936	BC002936 Homo sapi	466	23	2.0	4596	3	AF310896	AF310896 Dictyoste
394	23	2.0	1791	8	ATALLXSN	X92510 A. thaliana	467	23	2.0	4764	9	HSU0802806	AF310896 Dictyoste
395	23	2.0	1796	9	BC007064	BC007064 Homo sapi	468	23	2.0	5142	9	AK000086	AL390149 Homo sapi
396	23	2.0	1799	9	AF035284	AF035284 Homo sapi	469	23	2.0	5541	9	HSU080086	AK000086 Homo sapi
397	23	2.0	1810	9	AF218011	AF218011 Homo sapi	470	23	2.0	7836	9	HSU080086	AK000086 Homo sapi
398	23	2.0	1828	3	CENCRAL	X83887 C. elegans m	471	23	2.0	9170	9	HSB33D11	AF157814 Homo sapi
399	23	2.0	1832	8	BJY10848	Y10848 Brassica ju	472	23	2.0	9521	6	ARI37242	AF157814 Homo sapi
400	23	2.0	1853	9	AY007104	AY007104 Homo sapi	473	23	2.0	10094	1	AE001498	AL008640 Human DNA
401	23	2.0	1872	3	AF070920	AF070920 Caenorhab	474	23	2.0	10094	1	AE001498	AL008640 Human DNA
402	23	2.0	1874	6	AX008640	AX008640 Sequence	475	23	2.0	11282	6	AC014906	AE001498 Helicobac
403	23	2.0	1886	8	AF215854	AF215854 Zea mays	476	23	2.0	11282	6	AC014906	AE001498 Helicobac
404	23	2.0	1886	8	BC004526	BC004526 Homo sapi	477	23	2.0	11282	6	AC014906	AE001498 Helicobac
405	23	2.0	1893	9	AF070573	AF070573 Homo sapi	478	23	2.0	11282	6	AC014906	AE001498 Helicobac
406	23	2.0	1896	9	BC007846	BC007846 Homo sapi	479	23	2.0	13535	3	AE001416	AX128601 Sequence
407	23	2.0	1914	9	HSU49396	U9396 Human Ionot	480	23	2.0	13535	3	AE001416	AX128601 Sequence
408	23	2.0	1948	10	AF260582	AF260582 Rattus no	481	23	2.0	13905	6	ARI37241	AX174827 Sequence
409	23	2.0	1978	9	AF016709	AF016709 Homo sapi	482	23	2.0	16392	9	ARI37241	AE001416 Plasmidiu
410	23	2.0	1986	9	HSU49395	U49395 Human Ionot	483	23	2.0	16556	6	AR043384	AL354745 Human DNA
411	23	2.0	2017	9	AB050415	AB050415 Macaca fa	484	23	2.0	16556	6	AR043384	AL354745 Human DNA
412	23	2.0	2051	10	AB041540	AB041540 Mus muscu	485	23	2.0	16556	6	AR043384	AL354745 Human DNA
413	23	2.0	2062	10	AB041550	AB041550 Mus muscu	486	23	2.0	18705	3	CEY26866A	AL354745 Human DNA
414	23	2.0	2064	9	HSU92544	U92544 Human hepat	487	23	2.0	20866	9	HSU51243	U51243 Human alpha
415	23	2.0	2069	9	AF339775	AF339775 Homo sapi	488	23	2.0	24454	4	SPAC6C3	Z69731 S. pombe chr
416	23	2.0	2077	9	BC000304	BC000304 Homo sapi	489	23	2.0	24643	8	CELF5AC4	AF099916 Caenorhab
417	23	2.0	2079	9	AB047878	AB047878 Macaca fa	490	23	2.0	27500	3	CELF5AC4	AF099916 Caenorhab
418	23	2.0	2092	9	HSU58089	U58089 Human Hs-cu	491	23	2.0	29442	9	AL355855	AL355855 Human DNA
419	23	2.0	2108	9	BC010743	BC010743 Homo sapi	492	23	2.0	29856	8	AC007311	AC007311 Arabidops
420	23	2.0	2133	6	A93395	A93395 Sequence 1	493	23	2.0	30824	9	AC016911	AC016911 Homo sapi
421	23	2.0	2185	10	BC005633	BC005633 Mus muscu	494	23	2.0	32256	2	AL513169	AL513169 Homo sapi
422	23	2.0	2203	9	AK025632	AK025632 Homo sapi	495	23	2.0	33782	3	CEZK909	Z82096 Caenorhabdi
423	23	2.0	2209	9	BC002471	BC002471 Homo sapi	496	23	2.0	33917	9	AC004410	AC004410 Homo sapi
424	23	2.0	2219	9	AF181875	AF181875 Homo sapi	497	23	2.0	34688	9	AC005759	AC005759 Homo sapi
425	23	2.0	2220	3	DFCAMP1	X52688 D. discoideu	498	23	2.0	35776	3	AF067946	AF067946 Caenorhab
426	23	2.0	2240	3	AF0635049	AF235049 Homo sapi	499	23	2.0	36302	3	CEXC482	Z93397 Caenorhabdi
427	23	2.0	2241	3	AF0635049	AF0635049 Homo sapi	500	23	2.0	37154	9	HS316G12	AF025467 Caenorhab
428	23	2.0	2255	3	AF201905	AF201905 Drosophill	501	23	2.0	37476	9	HS316G12	AF025467 Caenorhab
429	23	2.0	2262	3	AF132194	AF132194 Drosophill	502	23	2.0	38381	9	CEC54E10	CEC54E10 Homo sapi
430	23	2.0	2287	3	CSA307910	AJ307910 Cupienniu	503	23	2.0	38591	3	CEC54E10	CEC54E10 Homo sapi
431	23	2.0	2328	9	BC002791	BC002791 Homo sapi	504	23	2.0	39372	3	AL162911	AL162911 Human DNA
432	23	2.0	2367	9	HSU0801132	AL117598 Homo sapi	505	23	2.0	39434	9	AF006752	AF006752 Homo sapi
433	23	2.0	2373	6	I771100	I771100 Sequence 1	506	23	2.0	39835	9	AF006752	AF006752 Homo sapi
434	23	2.0	2393	9	BC001957	BC001957 Homo sapi	507	23	2.0	40910	2	AC005260	AC005260 Homo sapi
435	23	2.0	2455	5	AF022890	AF022890 Gallus ga	508	23	2.0	41132	2	AC022741	AC022741 Homo sapi

655	23	2.0	97385	9	HS04747F3	AL050348	Human DNA	738	23	2.0	113762	9	AC005294	Homo sapi
656	23	2.0	97845	9	AL355337	AL355337	Human DNA	c 729	23	2.0	114003	9	AC008547	Homo sapi
657	23	2.0	98329	9	AL390295	AL390295	Human DNA	730	23	2.0	114149	9	AC022083	Homo sapi
658	23	2.0	98362	9	AL390295	AL390295	Human DNA	c 731	23	2.0	114194	2	AC093200	Homo sapi
659	23	2.0	98393	9	AL356472	AL356472	Human DNA	732	23	2.0	114258	2	AP000671	Homo sapi
660	23	2.0	98593	2	AL356472	AL356472	Human DNA	c 733	23	2.0	114351	2	AC006875	Homo sapi
661	23	2.0	98876	9	HS04747F3	AL078461	Human DNA	c 734	23	2.0	114364	9	AC011666	Human Chr
662	23	2.0	99887	2	AC026481	AC026481	Human sapi	c 735	23	2.0	114526	9	HSJ1043F6	Human DNA
663	23	2.0	100000	9	AB020877	AB020877	Homo sapi	736	23	2.0	114842	9	AC002996	Homo sapi
664	23	2.0	100000	9	AP000035	AP000035	Homo sapi	737	23	2.0	115218	9	HS159A1	Human DNA
665	23	2.0	100000	9	AP000075	AP000075	Homo sapi	738	23	2.0	115304	9	AL138775	Human DNA
666	23	2.0	100000	9	AP000100	AP000100	Homo sapi	739	23	2.0	115327	2	AL591381	Homo sapi
667	23	2.0	100000	9	AP000127	AP000127	Homo sapi	c 740	23	2.0	117502	9	AP000442	Homo sapi
668	23	2.0	100000	9	AP000176	AP000176	Homo sapi	741	23	2.0	117602	2	AC007055	Homo sapi
669	23	2.0	100000	9	AP000205	AP000205	Homo sapi	c 742	23	2.0	118195	9	AC007899	Homo sapi
670	23	2.0	100288	2	AP001945	AP001945	Homo sapi	743	23	2.0	118357	9	HS1142C11	Human DNA
671	23	2.0	100296	9	AL590308	AL590308	Human DNA	744	23	2.0	118524	9	AL121950	Human DNA
672	23	2.0	100925	9	AC012637	AC012637	Homo sapi	745	23	2.0	118595	9	AC002379	Human BAC
673	23	2.0	100983	2	AP003840	AP003840	Oryza sat	746	23	2.0	119349	9	AC020934	Homo sapi
674	23	2.0	101041	2	AP002079	AP002079	Homo sapi	747	23	2.0	119790	9	HS0989D7	Human DNA
675	23	2.0	101216	2	AC060227	AC060227	Homo sapi	748	23	2.0	120112	9	AC012355	Homo sapi
676	23	2.0	101245	2	AC079338	AC079338	Homo sapi	749	23	2.0	120829	2	AC009829	Homo sapi
677	23	2.0	101629	2	AC010023	AC010023	Drosophila	c 750	23	2.0	121086	5	AL590146	Human DNA
678	23	2.0	101685	9	HS039622	AL050341	Human DNA	751	23	2.0	121606	9	AL160401	Human DNA
679	23	2.0	101830	9	AL359454	AL359454	Human DNA	752	23	2.0	122103	9	HS291J10	Human DNA
680	23	2.0	102135	8	AC069144	AC069144	Arabidops	c 753	23	2.0	122638	9	AB001523	Homo sapi
681	23	2.0	102703	9	AC004910	AC004910	Homo sapi	c 754	23	2.0	122732	2	HS436C18	Homo sapi
682	23	2.0	103115	9	AC026440	AC026440	Homo sapi	c 755	23	2.0	123339	2	AF179296	Homo sapi
683	23	2.0	103153	9	AC010340	AC010340	Homo sapi	c 756	23	2.0	123695	9	HSJ581I13	Human DNA
684	23	2.0	103649	9	AL445219	AL445219	Homo sapi	c 757	23	2.0	124230	2	AL591742	Homo sapi
685	23	2.0	103740	9	HSJ102H19	AL096817	Human DNA	c 758	23	2.0	124439	2	AL603717	Homo sapi
686	23	2.0	103779	2	AC073239	AC073239	Homo sapi	759	23	2.0	124441	2	AC027098	Homo sapi
687	23	2.0	103788	9	AC008643	AC008643	Homo sapi	c 760	23	2.0	124667	2	AC015568	Homo sapi
688	23	2.0	103826	9	AL139339	AL139339	Human DNA	761	23	2.0	124845	2	AL353172	Homo sapi
689	23	2.0	104086	3	AE003567	AE003567	Drosophila	c 762	23	2.0	124876	9	AC004167	Homo sapi
690	23	2.0	104848	2	AC004588	AC004588	Homo sapi	763	23	2.0	124927	2	AC010475	Homo sapi
691	23	2.0	104913	9	AC004242	AC004242	Homo sapi	c 764	23	2.0	125000	9	AB017602	Homo sapi
692	23	2.0	105080	9	AC026439	AC026439	Homo sapi	765	23	2.0	125000	2	AL163540	Homo sapi
693	23	2.0	106168	9	AC011450	AC011450	Homo sapi	c 766	23	2.0	125295	2	AF186998	Homo sapi
694	23	2.0	106486	2	AC011805	AC011805	Homo sapi	c 767	23	2.0	125373	9	AL353707	Human DNA
695	23	2.0	106534	9	AL355609	AL355609	Human DNA	c 768	23	2.0	125376	9	AP001627	Homo sapi
696	23	2.0	106806	2	AF165177	AF165177	Homo sapi	769	23	2.0	125439	9	AC010485	Homo sapi
697	23	2.0	107159	9	HS422F24	AL031010	Human DNA	c 770	23	2.0	125653	9	AL133517	Human DNA
698	23	2.0	107264	9	AP002078	AP002078	Homo sapi	771	23	2.0	126266	2	AC008885	Homo sapi
699	23	2.0	107387	9	HS07K17	AL024473	Human DNA	772	23	2.0	126367	9	AL136109	Human DNA
700	23	2.0	107418	9	HS551E13	AL022163	Human DNA	c 773	23	2.0	126392	2	AC018785	Homo sapi
701	23	2.0	107429	9	HSJ214W20	AL121969	Human DNA	c 774	23	2.0	126392	2	AC018785	Homo sapi
702	23	2.0	108124	2	AL157948	AL157948	Homo sapi	c 775	23	2.0	126464	9	HS225E12	Human DNA
703	23	2.0	108765	2	AF216674	AF216674	Homo sapi	776	23	2.0	126883	2	AC008832	Homo sapi
704	23	2.0	108803	9	HS550H1	AL035420	Human DNA	777	23	2.0	127661	2	AP001261	Human DNA
705	23	2.0	109395	2	AC013742	AC013742	Homo sapi	c 778	23	2.0	127867	9	HS694B14	Human DNA
706	23	2.0	109723	2	AP000633	AP000633	Homo sapi	779	23	2.0	128289	9	AC007972	Homo sapi
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873 2.0 143405 2 AC062023 Homo sapi

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ALIGNMENTS

RESULT 1	AC064803/c	214005 bp	DNA	HTG	09-MAY-2001
LOCUS	AC064803	214005 bp	DNA	HTG	09-MAY-2001
DEFINITION	Mus musculus chromosome 11 clone RP23-16G14 map 11, WORKING DRAFT				
ACCESSION	SEQUENCE, 15 unordered pieces.				
VERSION	AC064803.3 GI:12061538				
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota: Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 214005)				
	Birren,B., Linton,L., Nusbaum,C. and Lander,E.				

Mus musculus chromosome 11, clone RP23-16G14

Unpublished
2 (bases 1 to 214005)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehotzky,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Melchior,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Submitted (22-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jan 10, 2001 this sequence version replaced gi:10122086.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9173

----- Summary Statistics

Sequencing vector: M13; M7815; 55% of reads

Sequencing vector: Plasmid; n/a; 45% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 208302 bases at least Q40

Consensus quality: 210581 bases at least Q30

Consensus quality: 211578 bases at least Q20

Insert size: 197000; agarose-fp

Insert size: 212605; sum-of-contigs

Quality coverage: 8.3 in Q20 bases; agarose-fp

Quality coverage: 7.7 in Q20 ba.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 21460: contig of 21460 bp in length

* 21461 21560: gap of 100 bp

* 21561 24845: contig of 3285 bp in length

* 24846 24945: gap of 100 bp

* 24946 28115: contig of 3170 bp in length

* 28116 28215: gap of 100 bp

* 28216 36178: contig of 7963 bp in length

* 36179 36278: gap of 100 bp

* 36279 43409: contig of 7131 bp in length

* 43410 43509: gap of 100 bp

* 43510 52058: contig of 8549 bp in length

* 52059 52158: gap of 100 bp

* 52159 91851: contig of 39693 bp in length

* 91852 91951: gap of 100 bp

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* 91952 104472: contig of 12521 bp in length
* 10473 104572: gap of 100 bp
* 104573 117147: contig of 12575 bp in length
* 117148 117247: gap of 100 bp
* 117248 129469: contig of 12222 bp in length
* 129470 129569: gap of 100 bp
* 129570 143560: contig of 13991 bp in length
* 143561 143660: gap of 100 bp
* 143661 159711: contig of 16051 bp in length
* 159712 159811: gap of 100 bp
* 159812 178155: contig of 18344 bp in length
* 178156 178255: gap of 100 bp
* 178256 200956: contig of 22701 bp in length
* 200957 201056: gap of 100 bp
* 201057 214005: contig of 12949 bp in length.

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FEATURES

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201057..214005
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vector_side:right
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ORIGIN

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Query Match 2.6%; Score 30; DB 2: Length 214005;
 Best Local Similarity 100.08; Pred. No. 0.00021;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1144 tgagattatttcaaaaaaaaaaaaaaaaaa 1173
 |||||

Db 91303 TGAGATTATTTCAAAAAAAAAAAAAAAAA 91274

RESULT 2
 AC041023/C.
 LOCUS

22-MAY-2000

HTG

DNA

185996 bp

DEFINITION

Homo sapiens clone RP11-356G3, WORKING DRAFT SEQUENCE, 20 unordered pieces.

AC041023

VERSION AC041023.2 GI:8016758

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 185996)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-356G3

Unpublished

2 (bases 1 to 185996)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhgaltier, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAtellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 22, 2000 this sequence version replaced gi:7534225.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9601

Center clone name: 355_G_3

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 175155 bases at least Q40

Consensus quality: 180623 bases at least Q30

Consensus quality: 182712 bases at least Q20

Insert size: 188000; agarose-fp

Insert size: 184096; sum-of-contigs

Quality coverage: 4.5 in Q20 bases; agarose-fp

Quality coverage: 4.6 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2941: contig of 2941 bp in length

2942 3041: gap of 100 bp

3042 5193: contig of 2152 bp in length

mat_pe

80. .421

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SDIDTNNNNNNNNSSODNNNNNNNNKKQKNGIKLFIGGINFDLKG
EOLKOIRQKLIHLFQSGVLKTSYHWDKGYFFISYNNKYVSQTVDSEFTTKRQK
YIDKIKDLKSEKCATPOLNFRPFPNYSVSAKNSGKQ"

BASE COUNT      943 a      291 c      240 g      1044 t
ORIGIN

Query Match      2.2%; Score 26; DB 3; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
Db 1555 ATTATTTCAAAAAA 1580
|||||

RESULT 5
AF145620 mRNA INV 14-JUN-1999
LOCUS Drosophila melanogaster clone GH03922 BCDNA.GH03922)
DEFINITION mRNA, complete cds.
ACCESSION AF145620.1 GI:5052529
VERSION FLI.CDNA.
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2580)
AUTHORS Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Frise,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Swirskas,R.R., Weinburg,T. and Celniker,S.E.
Full length Drosophila melanogaster cDNA sequence
Unpublished
JOURNAL 2 (bases 1 to 2580)
REFERENCE Rubin,G.M., Wan,K.H., Harvey,D., Lewis,S.E., Brokstein,P.,
Tsang,G., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Doyle,C.M.,
Farfan,D.E., Frise,E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Evans-Holm,M., Houston,K.A., Hummasti,S.R., Kim,E.,
Li,P., Moshrefi,M., Pacleb,J.M., Park,S., Sequeira,A., Sethi,H.,
Snir,E., Swirskas,R.R., Weinburg,T. and Celniker,S.E.
Direct Submission
JOURNAL Submitted (23-APR-1999) Berkeley Drosophila Genome Project,
University of California Berkeley, Berkeley, CA 94720, USA
COMMENT For further information about this sequence, including its location
and relationship to other sequences, please visit our web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu
FEATURES
source
1. .2580
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH03922"
1. .2580
/gene="BCDNA.GH03922"
63. .2312
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/codon_start=1
/product="BCDNA.GH03922"
/protein_id="RAD38595.1"

BASE COUNT      207 a      104 c      99 g      192 t
ORIGIN

Query Match      2.2%; Score 26; DB 8; Length 602;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
Db 577 ATTATTTCAAAAAA 602
|||||

RESULT 4
AF309947 DNA INV 06-MAR-2001
LOCUS Dictyostelium discoideum Rac1A (rac1A) gene, complete cds; and
DEFINITION unknown gene.
ACCESSION AF309947
VERSION AF309947.1 GI:12007269
KEYWORDS Dictyostelium discoideum.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE 1 (bases 1 to 2518)
AUTHORS Rivero,F., Dislich,H., Glockner,G. and Noegel,A.A.
TITLE The Dictyostelium discoideum family of Rho-related proteins
JOURNAL Nucleic Acids Res. 29 (5), 1068-1079 (2001)
MEDLINE 21127961
REFERENCE 2 (bases 1 to 2518)
AUTHORS Rivero,F., Dislich,H. and Noegel,A.A.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-2000) Institut fuer Biochemie I, Medizinische
Fakultaet, Universitaet zu Koeln, Joseph-Stelzmann-St. 52, Cologne
50931, Germany
FEATURES
source
1. .2518
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
Join(83. .164,299. .356,501. .841,961. .1462)
/gene="rac1A"
/product="Rac1A"
83. .1462
/gene="rac1A"
Join(350. .356,501. .841,961. .1197)
/codon_start=1
/product="Rac1A"
/protein_id="AAG45106.1"
/db_xref="GI:12007270"
/translation="MQAIKCVVGDGAVKTKLLISYTNNAFGVEYIPVFDNYSANV
MVDGKINGLMDTAQOEDYDLRLPSYPQTDVFLICFSIISPSFENYNGKWHPEIC
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TQRLKTVFDEAIRAVINPPLSKKKSSGCGNL"
misc_difference 1095
/gene="rac1A"
/note="compared to GenBank Accession Number L11588;
results in glutamate to glutamine substitution; Rac1B and
Rac1C also contain this substitution"
/replaces="c"
1335. .1340
/gene="rac1A"
/evidence=not_experimental
1382. .1387
/gene="rac1A"
/evidence=not_experimental
1424. .1429
/gene="rac1A"
/evidence=not_experimental
complement(join(<1809. .2019,2120. .>2518))
/product="unknown"
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/db_xref="FLYBASE:FBcd0003922"
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MGAGAGAGQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
MYGPGGPGGPAVGGAGGPAAGAGGPGNQMGQPMNVNMAQMPMQQIQQNLQGM
GNPNRMGQNGMGPGQMGQMGQMGQMGQMGQMGQMGQMGQMGQMGQMGQMGQ
GNPNMGCVGNPNPQKPNMPCQACQMGQMGQMGQMGQMGQMGQMGQMGQMGQ
AQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
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LDGTVNEMTKSKLETLICPTQVPLETLKCEKALEKMDLISYSGQFGKSNLS
NVTITLQSPVANHTYRTPTLELLFGDITAPVPAKRPVREKSTSEQGVPHV
LQGETARLDTFKFKLDTTSOINNAKIRLICLDKRLSPVPSVSPVEYPCQAPD
CSLAQEQYSNPFQTVQQAALIRLSKLPKNYSLLDWTWEMAVRQACSPQSPRAV
CELSYLLG"
BASE COUNT      741 a   645 c   667 g   527 t
ORIGIN

Query Match      2.2%; Score 26; DB 3; Length 2580;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attattcaaaaaaa 1173
|||||
Db 2547 ATTATTTCAAAAAA 2572

RESULT 6
HSM802758      5575 bp mRNA PRI 20-JUL-2000
LOCUS Homo sapiens mRNA; cDNA DKF2p761P06121 (from clone DKF2p761P06121).
DEFINITION AL390127
ACCESSION AL390127.1 GI:9368821
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 5575)
JOURNAL Poustka A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann, S.
COMMENT Direct Submission
Submitted (15-JUL-2000) MIPS, Am Klopferspitze 18a, D-82152
Martinsried, GERMANY
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKF2p761P06121) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES
Location/Qualifiers
source 1..5575
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p761P06121"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites Noti + SalI"
/dev_stage="adult"
/tissue_type="amygdala"
polyA_signal 5532..5537
polyA_site 5556
BASE COUNT      1225 a   1431 c   1557 g   1362 t
ORIGIN

Query Match      2.2%; Score 26; DB 9; Length 5575;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/db_xref="FLYBASE:FBcd0003922"
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GNPNMGCVGNPNPQKPNMPCQACQMGQMGQMGQMGQMGQMGQMGQMGQMGQ
AQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
QNSQNRQQSASINTPGVNTSPNQEEALIREKYKOLTKYIEPLKRLMAKIS
LDGTVNEMTKSKLETLICPTQVPLETLKCEKALEKMDLISYSGQFGKSNLS
NVTITLQSPVANHTYRTPTLELLFGDITAPVPAKRPVREKSTSEQGVPHV
LQGETARLDTFKFKLDTTSOINNAKIRLICLDKRLSPVPSVSPVEYPCQAPD
CSLAQEQYSNPFQTVQQAALIRLSKLPKNYSLLDWTWEMAVRQACSPQSPRAV
CELSYLLG"
BASE COUNT      741 a   645 c   667 g   527 t
ORIGIN

Query Match      2.2%; Score 26; DB 3; Length 2580;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attattcaaaaaaa 1173
|||||
Db 2547 ATTATTTCAAAAAA 2572

RESULT 6
HSM802758      5575 bp mRNA PRI 20-JUL-2000
LOCUS Homo sapiens mRNA; cDNA DKF2p761P06121 (from clone DKF2p761P06121).
DEFINITION AL390127
ACCESSION AL390127.1 GI:9368821
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 5575)
JOURNAL Poustka A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann, S.
COMMENT Direct Submission
Submitted (15-JUL-2000) MIPS, Am Klopferspitze 18a, D-82152
Martinsried, GERMANY
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKF2p761P06121) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES
Location/Qualifiers
source 1..5575
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2p761P06121"
/clone_lib="761 (synonym: hamy2). Vector pSport1; host
DH10B; sites Noti + SalI"
/dev_stage="adult"
/tissue_type="amygdala"
polyA_signal 5532..5537
polyA_site 5556
BASE COUNT      1225 a   1431 c   1557 g   1362 t
ORIGIN

Query Match      2.2%; Score 26; DB 9; Length 5575;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1148 attattcaaaaaaa 1173
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Db 5549 ATTATTTCAAAAAA 5574

RESULT 7
PFMAL4P1_0/c
WPCOMMENT
Sequence split into 4 fragments LOCUS PFMAL4P1 Accession AL034557
Fragment Name Begin End
PFMAL4P1_0 1 110000
PFMAL4P1_1 100001 210000
PFMAL4P1_2 200001 310000
PFMAL4P1_3 300001 392633
LOCUS PFMAL4P1 392633 bp DNA HTG 11-AUG-1999
DEFINITION Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL034557
VERSION 7 GI:5731897
KEYWORDS HTG: HTGS, PHASE1.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS 1 (bases 1 to 392633)
Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M.
and Barrell, B.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1998) P. falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
COMMENT On Aug 12, 1999 this sequence version replaced gi:5531346.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/projects/p.falciparum. IMPORTANT: This
sequence is unfinished and does not necessarily represent the
correct sequence. Work on the sequence is in progress and the
release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc.
Order of segments is not known: 800 n's separate segments.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
FEATURES
Location/Qualifiers
source 1..392633
/organism="Plasmodium falciparum"
/strain="3D7"
/db_xref="taxon:5833"
/Chromosome="4"
BASE COUNT 146453 a 41490 c 42490 g 138992 t 23208 others
ORIGIN

Query Match      2.2%; Score 26; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attattcaaaaaaa 1173
|||||
Db 6518 ATTATTTCAAAAAA 6493

RESULT 8
AC006280/c
LOCUS AC006280 163443 bp DNA HTG 12-AUG-2000
DEFINITION Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
PROGRESS ***, 1 ordered pieces.
ACCESSION AC006280
VERSION AC006280.8 GI:9797728
KEYWORDS HTG: HTGS, PHASE2.
SOURCE malaria parasite P. falciparum.
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IKERGVDNSQIKVICAVGAPPALQKLEKFGPLGHVYAGILDPVTNDKGFIIPLGLDAG
DRSFGT"
polyA_site 1298
BASE COUNT 380 a 233 c 285 g 420 t
ORIGIN

Query Match 2.1%; Score 25; DB 8; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaaaaaaaaaa 1173
|||||
Db 1292 TTATTCAAAAAAAAAAAAAA 1316
|||||

RESULT 11
GGK60GENE 1445 bp mRNA VRT 01-JUN-1998
LOCUS Gallus gallus mRNA for K60 protein.
DEFINITION Y14971
ACCESSION Y14971
VERSION Y14971.1 GI:3175993
KEYWORDS K60 gene.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1445)
AUTHORS Sick,C.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1997) C. Sick, University of Freiburg, Department
of Virology, Hermann-Herder-Strasse 11, D-79008 Freiburg, FRG

REFERENCE 2 (bases 1 to 1445)
AUTHORS Sick,C.
JOURNAL Unpublished
FEATURES
source
1. .1445
Location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
/rearranged
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/clone_lib="LPS stimulated HD-11 cells cloned in pcDNA1"
sig_peptide 246. .305
CDS 246. .560
/gene="k60"
/notes="LPS induced in primary macrophages, belongs to the
C-X-C chemokine family"
/codon_start=1
/product="K60 protein"
/protein_id="CAA75212.1"
/db_xref="GI:3175994"
/db_xref="SPTREMBL:O73912"
/translation="WMGKAVAAVMALLITSMAGKGMQAQARSAILRQCQIETHSKFTI
HPKFIQNVLTSPGPHCKNVEIATLKDGRECLDPTAPVKKLIKAILDKADTNKT
AS"
gene 246. .560
/mat_peptide 306. .557
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/product="K60 protein"
BASE COUNT 443 a 295 c 297 g 410 t
ORIGIN

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Query Match 2.1%; Score 25; DB 5; Length 1445;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaaaaaaaaaa 1173
|||||
Db 1421 TTATTCAAAAAAAAAAAAAA 1445
|||||

RESULT 12
CE19144 1498 bp DNA INV 21-JUN-2000
LOCUS Ceratitis capitata mssp-al gene for male specific serum polypeptide
DEFINITION alpha 1.
ACCESSION Y19144
VERSION Y19144.1 GI:6682266
KEYWORDS male specific serum polypeptide alpha 1; mssp-al gene.
SOURCE Mediterranean fruit fly.
ORGANISM Ceratitis capitata
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Tephritoidea; Tephritidae; Ceratitidae.
REFERENCE 1 (bases 1 to 1498)
AUTHORS Christophides,G.K., Mintzas,A.C. and Komitopoulou,K.
TITLE Organization, evolution and expression of a multigene family
encoding putative members of the odourant binding protein family in
the medfly Ceratitis capitata
JOURNAL Insect Mol. Biol. 9 (2), 185-195 (2000)
MEDLINE 20225580
REFERENCE 2 (bases 1 to 1498)
AUTHORS Komitopoulou,K.S.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1999) K.S. Komitopoulou, University of Athens,
School of Biological Sciences, Panepistimiopolis, Kouponia 15701,
Athens, GREECE
FEATURES
source
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Location/Qualifiers
/organism="Ceratitis capitata"
/db_xref="taxon:7213"
TATA_signal 429. .434
gene 429. .1430
/genes="mssp-al"
CDS join(499. .537,954. .1349)
/genes="mssp-al"
/codon_start=1
/product="male specific serum polypeptide alpha 1"
/protein_id="CAB64651.1"
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/db_xref="SPTREMBL:Q9U3T0"
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ELOKQEDNLDPSDDTVRKVEVCVFRKWIIDAEDNFHGRVLKQFDVLDVEVNIQ
KVNNCVDKNEQGSPIDVYASRIQRCIDKTDIAPNLLKVGKL"
499. .537
/genes="mssp-al"
/number=1
intron 538. .953
/genes="mssp-al"
/number=1
exon 954. .1349
/genes="mssp-al"
/number=2
polyA_signal 1425. .1430
/genes="mssp-al"
BASE COUNT 549 a 228 c 292 g 429 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1498;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 846 TTATTTCAAAAAAAAAAAAAAAAA 870

RESULT 13
LOCUS CCA19145 1572 bp DNA INV 21-JUN-2000
DEFINITION Ceratitis capitata mssp-a2 gene for male specific serum polypeptide
alpha 2.
ACCESSION Y19145 GI:6682268
KEYWORDS male specific serum polypeptide alpha 2; mssp-a2 gene.
SOURCE Mediterranean fruit fly.
ORGANISM Ceratitis capitata
REFERENCE 1 (bases 1 to 1572)
AUTHORS Christophides,G.K., Mintzas,A.C. and Komitopoulou,K.
TITLE Organization, evolution and expression of a multigene family
encoding putative members of the odourant binding protein family in
the medfly Ceratitis capitata
JOURNAL Insect Mol. Biol. 9 (2), 185-195 (2000)
MEDLINE 20225580
REFERENCE 2 (bases 1 to 1572)
AUTHORS Komitopoulou,K.S.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1999) K.S. Komitopoulou, University of Athens,
School of Biological Sciences, Panepistimiopolis, Kouponia 15701,
Athens, GRECE

FEATURES
source Location/Qualifiers
1. .1572
/organism="Ceratitis capitata"
/db_xref="taxon:7213"
/tissue_type="fat body"
492..497
/gene="mssp-a2"
492..1504
/gene="mssp-a2"
join(562..600,1028..1423)
/gene="mssp-a2"
/codon_start=1
/product="male specific serum polypeptide alpha 2"
/protein_id="CA864845.1"
/db_xref="GI:6682269"
/db_xref="SPTREMBL:Q9U3T9"
/translation="MKYFIVILAAVLAQAADDWPKTPEEFNAIRRECHKEFPFSK
ELQKEEIDFSDTEVRKYEVCFRKWGIIDADDFHGERLVKQFEAVLDGVEGIEQ
KVNCVDKNEQGSPIDVYASRIQQCIDKTDIAPKLLKLVIGKL"
562..600
/gene="mssp-a2"
/number=1
601..1027
/gene="mssp-a2"
/number=1
1028..1423
/gene="mssp-a2"
/number=2
1499..1504
/gene="mssp-a2"

BASE COUNT 596 a 235 c 298 g 443 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1572;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 913 TTATTTCAAAAAAAAAAAAAAAAA 937

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RESULT 14
LOCUS AK026358 1633 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ22705 fis, clone HSI13142.
ACCESSION AK026358
VERSION AK026358.1 GI:10439199
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI
clone:HSI13142.
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Kawabata,A., Hiki,j., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
AUTHORS 2 (bases 1 to 1633)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source Location/Qualifiers
1. 1633
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI13142"
/clone_lib="HSI"
/tissue_type="human small intestine"
/note="cloning vector pME18SFL3"

BASE COUNT 543 a 241 c 272 g 577 t
ORIGIN

Query Match 2.1%; Score 25; DB 9; Length 1633;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaa 1172
Db 1609 ATTATTTCAAAAAAAAAAAAAAAAA 1633

RESULT 15
LOCUS AF057693 1683 bp mRNA INV 19-JUN-2001
DEFINITION Sacculina carcini engrailed-a homeobox protein (en-a) mRNA,
en-a-E20 allele, complete cds.
ACCESSION AF057693
VERSION AF057693.1 GI:3746523
KEYWORDS Sacculina carcini.
ORGANISM Sacculina carcini
REFERENCE 1 (bases 1 to 1683)
AUTHORS Queinnee,E., Mouchel-Vielh,E., Guimonneau,M., Gibert,J.M.,
Turquier,Y. and Deutsch,J.S.
TITLE Cloning and expression of the engrailed.a gene of the barnacle

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JOURNAL      Sacculina carcini
MEDLINE      Dev. Genes Evol. 209 (3), 180-185 (1999)
PUBMED      99180702
REFERENCE    2 (bases 1 to 1683)
AUTHORS      Queinnee, E., Mouchel-Vielh, E., Guimonneau, M., Gibert, J.-M.,
              Turquier, Y., and Deutsch, J.S.
TITLE        Direct Submission
JOURNAL      Submitted (06-APR-1998) Developpement et Evolution, CNRS UMR7722, 9
              quai saint Bernard, Paris 75005, France
FEATURES     Location/Qualifiers
source       1. .1683
              /organism="Sacculina carcini"
              /db_xref="taxon:51650"
gene         1. .1683
              /gene="en-a"
              /allele="en-a-E20"
              55. .1020
              /gene="en-a"
              /codon_start=1
              /product="engrailed-a homeobox protein"
              /protein_id="AAC63993.1"
              /db_xref="GI:3746524"
              /translation="MGVQCEDSAAGLSLRPGDPSAPASARATTLSPRLLDGHT
              RQVTLGVNVRGGEDETRSPSTNLNFSIDNLRDFRGVCAIKSVQECRVPLPH
              HLPTHHHLLPRLPSSRLSASPVDLSSARVPKQOQOQKCPDNTA
              EVKRGSGASTAVDPERLANPALDADKKMPAWYCTRYSDRFSRGRVSRKT
              DEKRPRTAFSSQLRASEFTDNYRLSEERRORLAROLGNEISQIKIWFONKRAKLE
              KTRPDKPSLAKKLMQGLYHTTILPEDEKLMOLYKOSAPHISV"
BASE COUNT   476 a 439 c 367 g 401 t
ORIGIN

Query Match      2.1%; Score 25; DB 3; Length 1683;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
      |||||
Db 1647 TTATTTCANAAAAAAAAAAAAAAAAA 1671

RESULT 16
DDU20806/c      1705 bp      DNA      INV      20-JUL-1996
LOCUS           Dictyostelium discoideum guanine nucleotide-binding protein alpha
DEFINITION      subunit 5 (G alpha 5) gene, complete cds.
ACCESSION       U20806
VERSION          U20806.1 GI:687740
KEYWORDS         Dictyostelium discoideum.
SOURCE           Dictyostelium discoideum.
ORGANISM         Dictyostelium discoideum.
REFERENCE        1 (bases 1 to 1705)
AUTHORS          Hadwiger, J.A., Natarajan, K. and Firtel, R.A.
TITLE            Mutations in the Dictyostelium heterotrimeric G protein alpha
                  subunit G alpha5 alter the kinetics of tip morphogenesis
JOURNAL          Development 122 (4), 1215-1224 (1996)
MEDLINE          96205045
REFERENCE        2 (bases 1 to 1705)
AUTHORS          Hadwiger, J.A.
TITLE            Direct Submission
JOURNAL          Submitted (09-FEB-1995) Jeffrey A. Hadwiger, Microbiology and
                  Molecular Genetics, Oklahoma State University, 306 Life Sciences
                  East, Stillwater, OK 74078, USA
FEATURES         Location/Qualifiers
source           1. .1705
                  /organism="Dictyostelium discoideum"
                  /db_xref="taxon:44689"
exon             1. .391
5'UTR            1. .100
gene             join(101. .391,776. .930,1040. .1637)
                  /gene="G alpha 5"

JOURNAL      Sacculina carcini
MEDLINE      Dev. Genes Evol. 209 (3), 180-185 (1999)
PUBMED      99180702
REFERENCE    2 (bases 1 to 1683)
AUTHORS      Queinnee, E., Mouchel-Vielh, E., Guimonneau, M., Gibert, J.-M.,
              Turquier, Y., and Deutsch, J.S.
TITLE        Direct Submission
JOURNAL      Submitted (06-APR-1998) Developpement et Evolution, CNRS UMR7722, 9
              quai saint Bernard, Paris 75005, France
FEATURES     Location/Qualifiers
source       1. .1683
              /organism="Sacculina carcini"
              /db_xref="taxon:51650"
gene         1. .1683
              /gene="en-a"
              /allele="en-a-E20"
              55. .1020
              /gene="en-a"
              /codon_start=1
              /product="engrailed-a homeobox protein"
              /protein_id="AAC63993.1"
              /db_xref="GI:3746524"
              /translation="MGVQCEDSAAGLSLRPGDPSAPASARATTLSPRLLDGHT
              RQVTLGVNVRGGEDETRSPSTNLNFSIDNLRDFRGVCAIKSVQECRVPLPH
              HLPTHHHLLPRLPSSRLSASPVDLSSARVPKQOQOQKCPDNTA
              EVKRGSGASTAVDPERLANPALDADKKMPAWYCTRYSDRFSRGRVSRKT
              DEKRPRTAFSSQLRASEFTDNYRLSEERRORLAROLGNEISQIKIWFONKRAKLE
              KTRPDKPSLAKKLMQGLYHTTILPEDEKLMOLYKOSAPHISV"
BASE COUNT   476 a 439 c 367 g 401 t
ORIGIN

Query Match      2.1%; Score 25; DB 3; Length 1705;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
      |||||
Db 1647 TTATTTCANAAAAAAAAAAAAAAAAA 1671

RESULT 17
OYV15993        1891 bp      mRNA      INV      28-DEC-1997
LOCUS           Onchocerca volvulus mRNA for novel antigen, clone OV-47.
DEFINITION      Onchocerca volvulus mRNA for novel antigen, clone OV-47.
ACCESSION       Y15993
VERSION          Y15993.1 GI:2739313
KEYWORDS         antigen.
SOURCE           Onchocerca volvulus.
ORGANISM         Onchocerca volvulus.
REFERENCE        1 (bases 1 to 1891)
AUTHORS          Titanji, V.P.K., Sakwe, A.M., Chogomu, S.M., Souopgui, J., Djokam, R.T.,
                  Perlier, F. and Rask, D.
TITLE            A cDNA coding for a novel antigen from Onchocerca volvulus
JOURNAL          Unpublished
AUTHORS          Sakwe, A.
TITLE            Direct Submission
JOURNAL          Submitted (19-DEC-1997) A. Sakwe, Biotechnology Centre, University
                  of Yaounde, Department of Life Sciences, Faculty of Science,
                  University of Buera, P.O. Box 63, Buera, CAMEROON
COMMENT          The clone was selected by screening an Onchocerca volvulus lambda
                  gt11 expression cDNA library prepared from adult female worms
                  (Francine
                  Perlier, unpublished) using a rabbit antiserum to the adult female
                  surface
                  proteins. This antiserum which recognised about a dozen O. volvulus
                  polypeptides was shown to be active in mediating leucocyte
                  adherence and
                  cytotoxicity to O. volvulus microfilariae. The product of the cloned
                  gene has
                  been expressed in E. coli and found to react strongly with
                  oncocercalasis
                  patient serum pools from patients with varying skin microfilaria
                  density.
FEATURES         Location/Qualifiers
source           1. .1891
                  /organism="Onchocerca volvulus"
                  /strain="Forest"

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/db_xref="taxon:6282"
/sex="female"
/clone.lib="lambda gt11"
/clone="OV-47"
/dev_stage="adult"
10..1089
/codon_start=1
/product="antigen"
/protein_id="CAA75924.1"
/db_xref="GI:2739314"
/db_xref="SPTREMBL:O46146"
/translation="MSHLSIYNLSHLLIKLIYCIILQSQALRINTGWSRRNQPS
ILAKFGQIDPLDAEHSRFGVGNVSPPIINGARGVLLIVPKTLVNGFLNKATLEOS
CDSLQNTSLFAEACLSGKDDVMRIPCPAGKLCVEEDPEKVINDSOMTLRIEE
PSAPQWVIVVACVLDIHLCKSVKVEIVHYDLMTNGSLPMLHYLNPFGYQSFEE
ONSARIYMLLFIITVVGFCOWRSVMLCNSASFFRHQLLNCIIVLTKFTGLTLCLNV
ITFSDGGGILFARLLGLRIARLMTCLLCILLISYGWSFGNSSEILLIYPKVVIWG
LITSARHFLFFINLHSLHLLTIIC"
polya_site
BASE COUNT 509 a 306 c 366 g 710 t
ORIGIN

Query Match 2.1%; Score 25; DB 3; Length 1891;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 1852 TTATTTCACAAAAA 1876

RESULT 18
XLU59483
LOCUS
DEFINITION Xenopus laevis putative transcription factor VegT (VegT) mRNA,
complete cds.
ACCESSION U59483
VERSION U59483.1
KEYWORDS GI:2725622
SOURCE African clawed frog.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Zhang, J. and King, M.L.
TITLE Xenopus VegT RNA is localized to the vegetal cortex during
oogenesis and encodes a novel T-box transcription factor involved
in mesodermal patterning
JOURNAL Development 122 (12), 4119-4129 (1996)
MEDLINE 97164724
REFERENCE 2 (bases 1 to 2691)
AUTHORS Zhang, J. and King, M.L.
TITLE Direct Submission
Submitted (29-MAY-1996) Department of Cell Biology and Anatomy
(R-124), University of Miami School of Medicine, 1600 NW 10 Avenue,
Miami, FL 33101, USA
COMMENT On Dec 29, 1997 this sequence version replaced gi:1698557.
FEATURES
source
1..2691
/organism="Xenopus laevis"
/db_xref="taxon:8355"
1..2691
/gene="VegT"
/notes="vegetally localized mRNA"
57..1424
/gene="VegT"
/notes="putative transcription factor"
/codon_start=1
/product="VegT"
/protein_id="AAB93301.1"
/db_xref="GI:2725623"

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/translation="MRNCRCEGLSAGHLEPEASNCASDVKSSPDMDSVSSQDSILYL
PNTVGASLEDQDLWSQFHQEGTEMITTKSRGRMFPOCKIRLFLGLHPYAKYMLLVDFVP
LDNFRYKWNKNQWEAAAGKAPHPPCRTYVHPDSPAPGAHMKDPCICFKLKLNTLID
QOQHILHSMHRYKPRFHVQSDMYNSPWGLVQVFSFPETFTSVAYQNEKITKLK
INHPFAKGFREOERSHKKRDDVLKILQOSPSKRQKKWEDSPADISDFPKAICVKE
ESTMDPAGYQNWVSDHEANQGLTPHSPESEGANQOQVPTSSSNFYNKSHYRRSSOH
LSSPFELGEPSSRLTPDIATVPDSDPDLSLAVFHVPTQNSAPERTCSMNFWEAPMK
QPLRGAMYSPYGADQWLVLPAQGYRPGVGTAYPTDLSLTOGAVAHPHSAMSQYSLSF
PYSCW"
BASE COUNT 753 a 574 c 612 g 752 t
ORIGIN

Query Match 2.1%; Score 25; DB 5; Length 2691;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2656 TTATTTCACAAAAA 2680

RESULT 19
XLU89707
LOCUS
DEFINITION Xenopus laevis Brachyury and Tbx related protein (Brat) mRNA,
complete cds.
ACCESSION U89707
VERSION U89707.1
KEYWORDS GI:1881739
SOURCE African clawed frog.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2703)
AUTHORS Horb, M.E. and Thomsen, G.H.
TITLE A vegetally-localized T-box transcription factor in Xenopus eggs
specifies mesoderm and endoderm and is essential for embryonic
mesoderm formation
JOURNAL Development (1997) In press
REFERENCE 2 (bases 1 to 2703)
AUTHORS Horb, M.E. and Thomsen, G.H.
TITLE Direct Submission
Submitted (14-FEB-1997) Biochemistry and Cell Biology, SUNY at
Stony Brook, Life Sciences 339, Stony Brook, NY 11794-5215, USA
FEATURES
source
1..2703
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="stage 10.5 gastrula"
/tissue_type="ventral mesoderm/endoderm"
1..2703
/gene="Brat"
80..1447
/gene="Brat"
/function="transcriptional activator"
/notes="T-box transcription factor; similar to Antipodean
encoded by GenBank Accession Number X99905 and Veg-T
encoded by GenBank Accession Number U59483"
/codon_start=1
/product="Brachyury and Tbx related protein"
/protein_id="AAB49478.1"
/db_xref="GI:1881740"
/translation="MRNCRCEGLSAGHLEPEASNCASDVKSSPDMDSVSSQDSILYL
PNTVGASLEDQDLWSQFHQEGTEMITTKSRGRMFPOCKIRLFLGLHPYAKYMLLVDFVP
LDNFRYKWNKNQWEAAAGKAPHPPCRTYVHPDSPAPGAHMKDPCICFKLKLNTLID
QOQHILHSMHRYKPRFHVQSDMYNSPWGLVQVFSFPETFTSVAYQNEKITKLK
INHPFAKGFREOERSHKKRDDVLKILQOSPSKRQKKWEDSPADISDFPKAICVKE
ESTMDPAGYQNWVSDHEANQGLTPHSPESEGANQOQVPTSSSNFYNKSHYRRSSOH
LSSPFELGEPSSRLTPDIATVPDSDPDLSLAVFHVPTQNSAPERTCSMNFWEAPMK
QPLRGAMYSPYGADQWLVLPAQGYRPGVGTAYPTDLSLTOGAVAHPHSAMSQYSLSF
PYSCW"

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BASE COUNT      747 a      583 c      617 g      756 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 5; Length 2703;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2679 TTATTTCACAAAAAAAAAAAAAAAAA 2703

RESULT 20
AF083225      2771 bp      mRNA      INV      11-MAR-1999
LOCUS      Caenorhabditis elegans nuclear receptor NHR-7 (nhr-7) mRNA,
DEFINITION      complete cds.
ACCESSION      AF083225
VERSION      AF083225.1 GI:4139075
KEYWORDS      Caenorhabditis elegans.
SOURCE      Caenorhabditis elegans.
ORGANISM      Caenorhabditis elegans
REFERENCE      1 (bases 1 to 2771)
AUTHORS      Sluder, A.E., Mathews, S.W., Hough, D., Yin, V.P. and Maina, C.V.
TITLE      The nuclear receptor superfamily has undergone extensive
            proliferation and diversification in nematodes
JOURNAL      Genome Res. 9 (2), 103-120 (1999)
MEDLINE      99148134
REFERENCE      2 (bases 1 to 2771)
AUTHORS      Sluder, A.E., Mathews, S.W., Yin, V.P., Hough, D. and Maina, C.V.
TITLE      Direct Submission
JOURNAL      Submitted (10-AUG-1998) New England Biolabs, 32 Tozer Rd., Beverly,
            MA 01915, USA

FEATURES
source
1..2771
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="IV"
/clone="Y72H7; Y51B3; Y37G7"
/notes="partial sequence obtained from EST clone yk396h7"
gene
1..2771
/gene="nhr-7"
1115..2725
/gene="nhr-7"
CDS
/codon_start=1
/product="nuclear receptor NHR-7"
/protein_id="AAD03683.1"
/db_xref="GI:4139076"
/translation="MGSYTRICAVGDPAPKIHGYVLACFCCKGFFRRAVKDGRNKY
VCFERKCEVTFERNACRYCFRKLVLGMNPDYVRPDREKSKGKTVLKKKSVSR
SUSYRADPDSFTLSPSRKLQSEIGKLAETCTSTNFDGIFSLKSLIADRSIA
RKTGSEADMCDSNPRQLNEQFGLIERIVQCVDYIDRLVLMLEERHCKFSVEDKSA
ISDTMHLHLLFSTSRFAVGAPGLDLKLSLAQLPCTHTLTKIADVFETYLKRP
STIEYSVLKAYIVLSAESVLSLSNESLSLARENLSELLFKVIKHSNKTISANS
LSLTLHFVYESNLSARIKQSQPFVRDSDPKIFPKILITDIINPEVSDLLTTANC
RLKLTQMGSLSSVPVPPSDTVLPHFSPSPSCQISAPPPQOQYDYSQMPST
SSYPANSPQSPFSPNLSSEPKPLEMTKSIIEFLRPNGMTTDMNKLKKNWADG
FRLTPVFNKDIYSQFFPELSNINQHHPF"
BASE COUNT      881 a      559 c      423 g      908 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 3; Length 2771;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2747 TTATTTCACAAAAAAAAAAAAAAAAA 2771

BASE COUNT      747 a      583 c      617 g      756 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 5; Length 2703;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2679 TTATTTCACAAAAAAAAAAAAAAAAA 2703

RESULT 21
PPRESAG1      3268 bp      DNA      INV      26-APR-1991
LOCUS      P.falciiparum FC27 RESA gene for ring-infected erythrocyte surface
DEFINITION      antigen.
ACCESSION      X04572
VERSION      X04572.1 GI:9960
KEYWORDS      antigen; ring-infected erythrocyte surface antigen; surface
            antigen.
SOURCE      malaria parasite P. falciiparum.
ORGANISM      Plasmodium falciiparum
REFERENCE      1 (bases 1 to 3268)
AUTHORS      Favaloro, J.M., Coppel, R.L., Corcoran, L.M., Foote, S.J., Brown, G.V.,
            Anders, R.F. and Kemp, D.J.
TITLE      Structure of the RESA gene of plasmodium falciiparum
JOURNAL      Nucleic Acids Res. 14 (21), 8265-8277 (1986)
MEDLINE      87066710
COMMENT      For 3' FC27 cDNA sequence see X05182, for overlapping NF7 cDNA
            sequence see X05181
Data kindly reviewed (10-JUL-1987) by Favaloro J.

FEATURES
source
1..3268
/organism="Plasmodium falciiparum"
/strain="FC27 (FCQ27/PNG Papua New Guinea isolate)"
/db_xref="taxon:5833"
/join(801..995,1199..3268)
/codon_start=1
/product="ring-infected erythrocyte surface antigen"
/protein_id="CAA28241.1"
/db_xref="GI:9961"
/db_xref="SWISS-PROT:P13830"
/translation="MRPHAYSWIFSSQOYMGTKVKEKNKPIYFSDDDEKRNKNSFL
KVLCKRGVLPIGLIYLILNGLNGYSSSGVQFTDRGRNLYGETLPVNPYADSE
EPNVVQVGLPFPEKFTLESPPDIIDHTNLGNEKFMPTDVRNRYNSNNYEAIPHIS
ENFLIVDKVLFDYNEKVDNLGRSGDDIIRKMQTLWDEIMDKRKYDSLEKQKTY
SKYQVDMKPEAVESKWTQCIKLTIDOGGENLEERLNSQFNKMYRQKYLNLKVRRLT
VLNOIAWKALSNQIYSCRKIMNSDISFKHINELKSLERHRAAKAAEAEMKKRAQKPK
KKSRGWLCCGGGDIETVEPQEPVQTVQEQVNYGDLPLSLASITNSAINTYD
TVKGYLDHETSADALYDEDLDFDLKQYMDLDTSEESVEEHEEHTVDDEHVE
EHTADDEHVEEPTVADEHVEPTVADEHVEPTVADEHVEPTVADEHVEPTVADEHVE
QTSAAAPTIEIDLYLDLGVDNADMEITERFKLAENYYPYQSGSTVFHNFKR
VNEAYQLGIDIDKRWYKGYGDIKQVNFNMPISIFVLLSLEKFKDFTGTPQITVTL
RFFFEKRLSMNDLENSEHLKFMQYQKREAHVSEVLLNLOPCITAGDSKNVPII
TKLELKGSRFDIPILESRLWIFKHVAKTHLKSSKSAKKLQQTQANKQELANINN
LMSTLKEVIGSGSEQ"
801..995
/product="put. signal peptide"
996..1198
/note="intron I"
2309..2515
/note="repetitious region 1"
BASE COUNT      1339 a      353 c      444 g      1132 t
ORIGIN
sig_peptide
intron
misc_feature
BASE COUNT      1339 a      353 c      444 g      1132 t
ORIGIN
Query Match
Best Local Similarity 100.0%; DB 3; Length 3268;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 1030 TTATTTCACAAAAAAAAAAAAAAAAA 1006

RESULT 22
A00661/c
LOCUS      A00661      4591 bp      DNA      PAT      09-JUL-1993
DEFINITION      P.falciiparum RESA gene for ring-infected erythrocyte surface
            antigen.
ACCESSION      A00661
VERSION      A00661.1 GI:410747

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repeat_region      /rpt_family="L1"
12291..12597
/rpt_family="Alu"
repeat_region      /rpt_family="L1"
12593..13092
/rpt_family="L1"
repeat_region      /rpt_family="Alu"
13163..13469
/rpt_family="Alu"
repeat_region      /rpt_family="L1MB3"
13465..13595
complement(14012..14151)
/rpt_family="Alu"
repeat_region      /rpt_family="L1"
14178..14470
complement(14691..14729)
note="GRAL1 2 excellent exon, frame 0"
14763..14818
/rpt_family="MIR"
15023..15163
note="51% protein identity HLA-DR B protein precursor"
repeat_region      /rpt_family="Alu"
15101..15564
/rpt_family="L1"
15243..15386
/rpt_family="L1"
17769..17858
/rpt_family="Alu"
17841..17860
note="(A)20"
/rpt_type=tandem
/rpt_unit=A
17870..18152
/rpt_family="Alu"
18175..18202
note="(AGG)7"
/rpt_type=tandem
/rpt_unit=AGG
19053..19350
/rpt_family="Alu"
BASE COUNT 5568 a 4820 c 5355 g 4670 t
ORIGIN

Query Match      2.1%; Score 25; DB 9; Length 20413;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaaa 1173
|||||
Db 2508 TTATTTCAAAAAAAAAAAAAAAAAAA 2532

RESULT 24
AC014449 AC014449 25147 bp DNA HTG 16-NOV-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
ACCESSION AC014449
VERSION AC014449.1 GI:6436886
KEYWORDS HTG: HTGS_PHASE2.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 25147)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10212978 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and

```

```

FEATURES
source
1..25147
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 6651 a 5450 c 5655 g 7391 t
ORIGIN

Query Match      2.1%; Score 25; DB 2; Length 25147;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaaa 1173
|||||
Db 19342 TTATTTCAAAAAAAAAAAAAAAAAAA 19366

RESULT 25
AC006540 AC006540 34000 bp DNA PRI 28-JUL-2000
LOCUS Homo sapiens chromosome 19, cosmid F23842, complete sequence.
DEFINITION AC006540
VERSION AC006540.2 GI:9558586
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 34000)
AUTHORS Lamerdin,J.E., McGready,P.M., Skowronski,E., Viswanathan,V.,
Burkhardt-Schultz,K.J., Gordon,L., Dias,J., Ramirez,M.,
Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A.,
Garnes,J., Dancanay,L., Erler,A., Christensen,M., Georgescu,A.,
Avila,J., Lib,S., Attix,C., Andreise,T., Frankheim,M.,
Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R.,
Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Brower,A.,
Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and
Carrano,A.V.
SEQUENCE ANALYSIS OF A 1.9 Mb region in 19q13.2 between APOE and
D19S412
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 34000)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1999) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
REFERENCE 3 (bases 1 to 34000)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2000) DOE Joint Genome Institute, Lawrence
Livermore National Laboratory, Livermore, CA 94550
On Jul 28, 2000 this sequence version replaced gi:4235139.
Map and sequence are oriented from centromere to q-telomere. This
accession represents bases 1 to 34,000 of the cosmid F23842 insert.
Cosmid F23842 (LNLNF-197C2) is overlapped on the left by BC34685.
(CTB-14D10, AC008623) from bases 1 to 18,432 of this accession, and
overlaps cosmid R30477 (LNLNR-266D1, AC011545) on the right from
bases 30,197 to 34,000 of this accession.
FEATURES
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/db_xref="taxon:9606"
/chromosome="19"
/map="19q13.2 between APOE and D19S412"
/clone="F23842"
/cell_line="UV5HL9-5B"
/clone_lib="L19NC02 F chromosome 19-specific cosmid
library"
/note="Cosmid library constructed at LLNL from flow-sorted
chromosomes from hybrid UV5HL9-5B, which carries
chromosome 19 as its only human chromosome."
misc_feature 28..833

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/note="DDS similarity to overlapping ESTs:
(388..28) R85163 y043b05.r1 Homo sapiens cDNA clone 180657
5'; (1..362) 98% identity.
(337..833) R55694 y988f12.r1 Homo sapiens cDNA clone 40397
5'; (1..517) 90% identity.
177..261
/note="predicted exon, program: graal2exons_human_1.3,
frame: 2, quality: excellent, score: 75.000"
complement(1178..1613)
/note="DDS similarity to R55695 y988f12.s1 Homo sapiens
cDNA clone 40397 3'; (1..439) 98% identity."
1566..1646
/rpt_family="POLY_A"
complement(join(1633..3065,15899..16065,23127..23271))
/product="Human putative astrocytic NOVA-like RNA-binding
protein (ANOVA) mRNA, partial cds"
1906..1967
/rpt_family="(GGA)n"
complement(join(1983..3065,15899..16065,23127..23271))
/note="astrocytic NOVA-like RNA-binding protein [Homo
sapiens]"
/codon_start=1
/product="RNA-binding protein Nova-2 [AA 29-492]"
/protein_id="AADI3116.1"
/db_xref="GI:4235140"
/translation="EEGEYPLKVLIPSYAAGSIIGKGGTIVLOKETGATIKLSKS
DEYPTGTERVCLVQGTAEALNAVHSPFAEKVRIPQAMTKPEVINLIQPTMTNPDRA
KQAKLVPNSTAGLIIKGKGTAVKAEQVQSGAWQVLSQKPEGINQERVVTVSGEPEQ
VHRAVAIVQGVQDPOSSCLNIPSNVAGPVANSPTGSPYASPADVLPAAASA
AASGLGPGAGLVAGFAAFPAFSGTDLLAISTALNTIASYNTNSIGLGNAAA
ASGVLAAGAAGAPAAANLILASAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
NGYLGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
ILGKGKTLVEYQELTGARLIQISKGEFLPGTNRNRTTNGSPATQAAYLISQVTV
YEOGVRASNPQKVG"
complement(2257..2373)
/rpt_family="(CGG)n"
2413..2534
/rpt_family="(CGG)n"
2711..2820
/rpt_family="(CGG)n"
2734..3065
/note="DDS similarity to Overlapping ESTs:
(3065..2734) AA904538 ok08f03.s1 Soares_NFL_T_GBC_S1 Homo
sapiens cDNA clone IMAGE:1507229 3' similar to
SW:NOAL_HUMAN P51513 ONCONEURAL VENTRAL ANTIGEN-1 ;
(331..1) 99% identity.
(2735..3091) AI077966 oy39c05.s1
Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:1668200 3' similar to SW:NOAL_HUMAN P51513
ONCONEURAL VENTRAL ANTIGEN-1 ; (1..356) 97% identity.
(3065..2736) W35411 zc08e08.s1 Soares_parathyroid tumor
NbHPA Homo sapiens cDNA clone 321734 3' similar to
PIR:A53184 A53184 myc
far upstream element-binding protein - human ; (328..1)
96% identity.
(3065..2752) AI040329 oy33b05.x1 Soares_parathyroid_t
umor_NbHPA Homo sapiens cDNA clone IMAGE:1667601 3'
similar to SW:NOAL_HUM
AN P51513 ONCONEURAL VENTRAL ANTIGEN-1 ; (314..1) 99%
identity.
and others."
complement(3092..3127)
/rpt_family="AT-rich"
3128..3430
/rpt_family="AluSx"
complement(3449..3577)
/rpt_family="AluJo"
3735..3861
/rpt_family="FLAM_C"
complement(4122..4193)
/rpt_family="MIR"
4271..4644
/rpt_family="MLT1B"

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complement(5174..5472)
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5553..5850
/rpt_family="AluJb"
5900..5936
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6278..6579
/rpt_family="AluJb"
6677..7001
/rpt_family="L1MB5"
6988..7101
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7144..7440
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7448..7546
/rpt_family="L1MB8"
complement(7558..7722)
/rpt_family="FRAM"
7726..7781
/rpt_family="L1MB7"
complement(7952..8063)
/rpt_family="AluSg/x"
8065..8141
/rpt_family="AluS"
8142..8433
/rpt_family="AluJb"
8442..8710
/rpt_family="L1MC4"
8712..9011
/rpt_family="AluSc"
complement(9027..9084)
/rpt_family="(CATG)n"
9165..9395
/rpt_family="LINE2"
complement(9592..9891)
/rpt_family="AluSg"
10021..10181
/rpt_family="MIR"
complement(10325..10373)
/rpt_family="LINE2"
10439..10739
/rpt_family="AluY"
10820..11435
/rpt_family="L1MB7"
11442..11476
/rpt_family="POLY_A"
11656..11777
/rpt_family="MIR"
complement(11860..12160)
/rpt_family="AluSx"
12175..12275
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complement(12282..12580)
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12877..12934
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complement(12936..13089)
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complement(13094..13192)
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13315..13454
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13455..13758
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13762..13918
/rpt_family="AluJb"
complement(13920..13949)
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complement(14297..14484)
/rpt_family="MIR"
14496..14644
misc_feature

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/note="BLASTN similarity to z57045 (84. .232); match: 0.99,

Query Match

Best Local Similarity 2.1%; Score 25; DB 9; Length 34000;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattcaaaaaa1173

Db 11435 TTATTTCAAAAA11459

RESULT 26

AC034287 43324 bp DNA HTG 26-FEB-2001
Mus musculus chromosome 11 clone RP23-239L6 map 11, LOW-PASS
SEQUENCE SAMPLING.
AC034287
AC034287.3 GI:13123926
HTG; HTGS_PHASE0.
house mouse.
Mus musculus
Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 43324)

2 (bases 1 to 43324)

3 (bases 1 to 43324)

4 (bases 1 to 43324)

5 (bases 1 to 43324)

6 (bases 1 to 43324)

7 (bases 1 to 43324)

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9 (bases 1 to 43324)

10 (bases 1 to 43324)

11 (bases 1 to 43324)

12 (bases 1 to 43324)

13 (bases 1 to 43324)

14 (bases 1 to 43324)

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49 (bases 1 to 43324)

50 (bases 1 to 43324)

51 (bases 1 to 43324)

52 (bases 1 to 43324)

53 (bases 1 to 43324)

* will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

* 1 675: contig of 675 bp in length

* 776 775: gap of 100 bp

* 1454 1454: contig of 679 bp in length

* 1455 1554: gap of 100 bp

* 1555 2252: contig of 698 bp in length

* 2253 2352: gap of 100 bp

* 2353 3021: contig of 669 bp in length

* 3022 3121: gap of 100 bp

* 3122 3804: contig of 683 bp in length

* 3805 3904: gap of 100 bp

* 3905 4583: contig of 679 bp in length

* 4584 4683: gap of 100 bp

* 4684 5365: contig of 682 bp in length

* 5366 5465: gap of 100 bp

* 5466 6156: contig of 691 bp in length

* 6157 6256: gap of 100 bp

* 6257 6951: contig of 695 bp in length

* 6952 7051: gap of 100 bp

* 7052 7734: contig of 683 bp in length

* 7735 7834: gap of 100 bp

* 7835 8516: contig of 682 bp in length

* 8517 8616: gap of 100 bp

* 8617 9303: contig of 687 bp in length

* 9304 9403: gap of 100 bp

* 9404 10080: contig of 677 bp in length

* 10081 10180: gap of 100 bp

* 10181 10866: contig of 686 bp in length

* 10867 10966: gap of 100 bp

* 10967 11666: contig of 700 bp in length

* 11667 11766: gap of 100 bp

* 11767 12454: contig of 688 bp in length

* 12455 12554: gap of 100 bp

* 12555 13246: contig of 692 bp in length

* 13247 13346: gap of 100 bp

* 13347 14025: contig of 679 bp in length

* 14026 14125: gap of 100 bp

* 14126 14884: contig of 759 bp in length

* 14885 14984: gap of 100 bp

* 14985 15672: contig of 688 bp in length

* 15673 15772: gap of 100 bp

* 15773 16463: contig of 691 bp in length

* 16464 16563: gap of 100 bp

* 16564 17234: contig of 671 bp in length

* 17235 17334: gap of 100 bp

* 17335 18038: contig of 704 bp in length

* 18039 18138: gap of 100 bp

* 18139 18836: contig of 698 bp in length

* 18837 18936: gap of 100 bp

* 18937 19636: contig of 700 bp in length

* 19637 19736: gap of 100 bp

* 19737 20416: contig of 680 bp in length

* 20417 20516: gap of 100 bp

* 20517 21224: contig of 708 bp in length

* 21225 21324: gap of 100 bp

* 21325 22003: contig of 679 bp in length

* 22004 22103: gap of 100 bp

* 22104 22792: contig of 689 bp in length

* 22793 22892: gap of 100 bp

* 22893 23580: contig of 688 bp in length

* 23581 23680: gap of 100 bp

* 23681 24384: contig of 704 bp in length

* 24385 24484: gap of 100 bp

* 24485 25199: contig of 715 bp in length

* 25200 25299: gap of 100 bp

* 25300 25956: contig of 657 bp in length

* 25957 26056: gap of 100 bp

* 26057 26726: contig of 670 bp in length

* 26727 26826: gap of 100 bp

* 26827 27504: contig of 678 bp in length

* 27505 27604: gap of 100 bp

TITLE
JOURNAL

COMMENT

Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 26, 2001 this sequence version replaced gi:10800291.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8880

Center clone name: 239_L-5

* NOTE: This record contains 55 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone


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CDS
TYNTLVLCFQSGKLNAAKELFQEMVSRGVPSPVVTYGIILLDGLDNGELNKALEIFE
KQKSKMTIGIYIIHGMCAASKVDWDAFLCSLSDKGVKPDVVTYINMIGLICK
KGLSADMLFRKMKEDGCTPDDEFYINILIRAHLGSGGLISSVELIEBMKVCGFSADS
STIKWIMLSDRRLDKSFLDMS"
6121.. 6567
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/protein_id="BAB01463.1"
/db_xref="GI:11994280"
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SEHSIVINAIQDQSKRCFRMIGGLVLTKEVLPVQRNKGSLGEEVVRKLYETLE
KKKDLTEPEAKYKIRITQEDNKGGNKEGNAQGVLVGRASSQ"
complement(join(6826..6990,7080..7385,7462..7779))
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/codon_start=1
/evidence=not_experimental
/product="seed maturation protein, LEA protein in group
5-like"
/protein_id="BAB01464.1"
/db_xref="GI:11994281"
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RVFGHTQKGAAYMSAATANKRGFVHPGDTDLAERGVTVTAQDVPGARVITEF
VGQVVGQVQPRVPAATAAMEAVVGLSQSAITIGALEATVYTAGNKPVDQSDAA
AIOAAEVACGTNVIAPGTIAASQAQSAANHNATIDREDKIKLIDVLGATGKLAADK
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8234.. 8563
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unknown protein"
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/db_xref="GI:11994282"
/translation="MLHERRLGVGRNQRTPTCATHKGRDVRVCEATYPRHWTR
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WKLRYF"
complement(join(8961..9125,9222..9515,9595..9906))
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MRASGTVNIALAGVASAASADHNATVDRDERKIKLRDLVLTGAAGKLSADRVTRED
AEGVSAEMRNPNKLCCTHPGGVAASLTVAARNLERVDI"
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gene_id:F16J14.8
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/db_xref="GI:11994284"
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PAIPVSTGGGLPYAPDPSGPDVWTVWRVGTAMGYHQDRFLILFORQOKRVPK
SFAPKPOLARYLESDFPDGADAFASFWSKVPALFQPAKPKYDAALFEETPEVQTE
VGQNDNAQDGKRSYRQKRPWPTQTYEVEAKPKSTPRSSNKKKKGATTPAT
GQOSTKPKPSQSGRTIOQGGAVDLNLFNEESEPAPAKTSNRKKRGVNYEE
EDYSIPIYVSPWNGVLAVHSPIDVNPPEFDSYLNLDNLMOQPEEVRDSSVLSV
VSSPREYEWAEARKISLLEKDTTLLFSDKAAEIALATKLKBDNLFAEEVLVL
KLMEETPSEVFQNGVIEADRFSALELNKAIVASLKYETISDLKEKLGSIQNEV
DYNSETIRIQDQIAQLQARSELKRYIGTKEKERVDSYQGMVANSIPKVQEVQS
ANLKPEWCECKDNALKREAEYLSTPLKGFLL"
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/notes="emb|CAB10262.1
gene_id:F16J14.9
similar to unknown protein"
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/db_xref="GI:11994285"
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LRSEADVAVEERHDCFRFAETVCLNGDCEMAYMVEIHGKITKIVRTNGSSSLGL
SLDELELDVWRFLPESTRPELVTVACVGDGLIVTPKNAEEDDDGGGDFQGGIGS
GRVLVQ"
complement(21274..21606)
/notes="gb|AAAF09050.1
gene_id:F16J14.10
similar to unknown protein"
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RSNTKLY"
complement(join(28868..28943,29119..29810))
/notes="gb|AAD31369.1
gene_id:F16J14.11
similar to unknown protein"
/codon_start=1
/evidence=not_experimental
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/notes="gene_id:F16J14.12"
/codon_start=1
/evidence=not_experimental
/product="alanine acetyl transferase-like protein"
/protein_id="BAB01471.1"
/db_xref="GI:11994288"
/translation="MIMESPRIFLRFNLSDAEDVFKWAGDDDVTRYLRWDSVNSLEE
AKOHILNKAIPHWRRSISLQDHSIGYVSRPDSGDRCDRADLAYAVAKEFWGRGI
ATAAVRMAVEQALEDFEVVRLQAVVEVENKASQVLEKAGFRKEGLEKYGFSKGTI
RDMFLYSVRDDCFV"
complement(join(36967..37029,37472..37671,37881..38202))

Query Match      2.1%; Score 25; DB 8; Length 47827;
Best Local Similarity 0.04; Pred. No. 0.096;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 35569 TTATTTCACAAAAAAAAAAAAAAAAA 35545

RESULT 28
HSDJ753M9 57698 bp DNA 12-DEC-1999
LOCUS
DEFINITION
Human DNA sequence from clone RPA-753M9 on chromosome 22 Contains
EST and STS, complete sequence.
ACCESSION
AL079301
VERSION
AL079301.14 GI:5725274
KEYWORDS
HTG.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37698)
Collier,R.
Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerquest@sanger.ac.uk
On Aug 10, 1999 this sequence version replaced gi:5668660.
This sequence has been finished according to sequence map criteria

```

as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/chr22>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

<http://www.sanger.ac.uk/Projects/C.elegans/wormpep> RP4-753M9 is from the library rPCI-4 constructed at the Roswell Park Cancer

Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone

RP4-753M9 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone XX-PRY7CC1 is at 57599 in this

sequence. The true right end of clone RP1-127B20 is at 100 in this sequence.

FEATURES

source	Location/Qualifiers
repeat_region	1..57698
repeat_region	/organism="Homo sapiens"
repeat_region	/db_xref="taxon:9606"
repeat_region	/chromosome="22"
repeat_region	/clone_lib="RPCI-4"
repeat_region	/clone="RP4-753M9"
repeat_region	1..148
repeat_region	/note="Charlie3 repeat: matches 1584..1728 of consensus"
repeat_region	155..1810
repeat_region	/note="Charlie3 repeat: matches 1..1681 of consensus"
repeat_region	1811..2136
repeat_region	/note="LIME3 repeat: matches 5589..5930 of consensus"
repeat_region	2353..2656
repeat_region	/note="AluSq repeat: matches 1..304 of consensus"
repeat_region	4059..4283
repeat_region	/note="MIR repeat: matches 12..262 of consensus"
repeat_region	5327..5857
repeat_region	/note="MIR repeat: matches 70..205 of consensus"
repeat_region	5658..6150
repeat_region	/note="MLT2CA repeat: matches 1..500 of consensus"
repeat_region	6151..6191
repeat_region	/note="MIR repeat: matches 205..244 of consensus"
repeat_region	8001..8160
repeat_region	/note="HAL1 repeat: matches 811..959 of consensus"
repeat_region	8196..8487
repeat_region	/note="AluSp repeat: matches 8..299 of consensus"
repeat_region	8794..8890
repeat_region	/note="HAL1 repeat: matches 269..372 of consensus"
repeat_region	8891..9232
repeat_region	/note="AluY repeat: matches 1..306 of consensus"
repeat_region	10366..10437
repeat_region	/note="L2 repeat: matches 2631..2701 of consensus"
repeat_region	10844..11248
repeat_region	/note="MLT2CB repeat: matches 1..430 of consensus"
repeat_region	11249..11544
repeat_region	/note="AluSg repeat: matches 3..298 of consensus"
repeat_region	11545..11558
repeat_region	/note="MLT2CB repeat: matches 430..442 of consensus"
repeat_region	11562..11850
repeat_region	/note="L1PA16 repeat: matches 5858..6157 of consensus"
repeat_region	11851..12164
repeat_region	/note="AluSk repeat: matches 1..310 of consensus"
repeat_region	12165..12558
repeat_region	/note="L1PA16 repeat: matches 5502..5858 of consensus"
repeat_region	12563..12578
repeat_region	/note="MLT2CB repeat: matches 429..442 of consensus"
repeat_region	12579..12920
repeat_region	/note="MER47A repeat: matches 1..365 of consensus"
repeat_region	12921..12972
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repeat_region	/note="MIR repeat: matches 20..262 of consensus"
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repeat_region	18621..18653
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repeat_region	18654..18956
repeat_region	/note="AluSk repeat: matches 1..303 of consensus"
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repeat_region	/note="L1MCB repeat: matches 147..537 of consensus"
repeat_region	24120..24247
repeat_region	/note="L2 repeat: matches 2383..2511 of consensus"
repeat_region	24424..24718
repeat_region	/note="AluJb repeat: matches 1..299 of consensus"
repeat_region	26177..26469
repeat_region	/note="AluSg repeat: matches 1..287 of consensus"
repeat_region	26472..26759
repeat_region	/note="L1MA6 repeat: matches 6009..6300 of consensus"
repeat_region	27151..27431
repeat_region	/note="AluJb repeat: matches 1..302 of consensus"
repeat_region	27572..27870
repeat_region	/note="AluSk repeat: matches 1..296 of consensus"
repeat_region	27623..27681
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repeat_region	27880..28177
repeat_region	/note="AluJb repeat: matches 1..291 of consensus"
repeat_region	28178..28549
repeat_region	/note="L1ME repeat: matches 5536..5944 of consensus"
repeat_region	28640..28950
repeat_region	/note="AluSk repeat: matches 1..312 of consensus"
repeat_region	29403..29464
repeat_region	/note="L2 repeat: matches 2638..2701 of consensus"
repeat_region	30073..30094
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repeat_region	31813..31896
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repeat_region	32948..33223
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* 22016 22723: contig of 708 bp in length
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Query Match          2.1%; Score 25; DB 2; Length 63331;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1149 ttattcaaaaaaaaaaaaaa 1173
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RESULT 30

AC090728

LOCUS 73880 bp DNA HTG 28-MAR-2001
DEFINITION Homo sapiens chromosome 15 clone RP11-507J18 map 15, LOW-PASS
SEQUENCE SAMPLING.

ACCESSION AC090728

VERSION AC090728.2 GI:13470213

KEYWORDS HTG; HTGS_PHASE0.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 73880)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 15, clone RP11-507J18

REFERENCE 2 (bases 1 to 73880)

Birren,B., Linton,L., Nusbaum,C.,

Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
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Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trioglio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (09-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 28, 2001 this sequence version replaced g1:13259447.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L12459

Center Clone name: 507_J_18

* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 747: contig of 747 bp in length
* 748 847: gap of 100 bp
* 848 1634: contig of 787 bp in length
* 1635 1734: gap of 100 bp
* 1735 2518: contig of 784 bp in length
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* 4277 4376: gap of 100 bp
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* 5168 5267: gap of 100 bp
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* 6048 6147: gap of 100 bp
* 6148 6919: contig of 772 bp in length
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* 7020 7837: contig of 818 bp in length
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* 15744 15843: gap of 100 bp
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* 21912 22011: gap of 100 bp
* 22012 22813: contig of 802 bp in length
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* 42185 42284: gap of 100 bp
* 42285 43066: contig of 782 bp in length
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* 44839 44938: gap of 100 bp
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* 51092 51191: gap of 100 bp
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* 58167 58266: gap of 100 bp
* 58267 59049: contig of 783 bp in length
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* 59150 59886: contig of 837 bp in length
* 59887 60086: gap of 100 bp
* 60087 60875: contig of 789 bp in length

Query Match
Best Local Similarity 100.0%; Pred. No. 0.09; Length 73880;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 14711 TTATTTCAAAAAAAAAAAAAAAAA 14735

RESULT 31
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DEFINITION Homo sapiens chromosome 8 clone RP11-714P7 map 8, LOW-PASS SEQUENCE
ACCESSION AC034306
VERSION AC034306.2 GI:7549708
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 81447)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-714P7
Unpublished
2 (bases 1 to 81447)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
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Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczek,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneau,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

```

COMMENT

On Apr 14, 2000 this sequence version replaced gi:7417884.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9350
 Center clone name: 714_P_7

* NOTE: This record contains 96 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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* 1 743: contig of 743 bp in length
* 744 843: gap of 100 bp
* 844 1596: contig of 753 bp in length
* 1597 1696: gap of 100 bp
* 1697 2393: contig of 697 bp in length
* 2394 2493: gap of 100 bp
* 2494 3243: contig of 750 bp in length
* 3244 3343: gap of 100 bp
* 3344 4094: contig of 751 bp in length
* 4095 4194: gap of 100 bp
* 4195 4917: contig of 723 bp in length
* 4918 5017: gap of 100 bp
* 5018 5747: contig of 730 bp in length
* 5748 5847: gap of 100 bp
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* 6999 7451: contig of 753 bp in length
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* 8408 9157: contig of 750 bp in length
* 9158 9257: gap of 100 bp
* 9258 10008: contig of 751 bp in length
* 10009 10108: gap of 100 bp
* 10109 10860: contig of 752 bp in length
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* 10961 11719: contig of 759 bp in length
* 11720 11819: gap of 100 bp
* 11820 12568: contig of 749 bp in length
* 12569 12668: gap of 100 bp
* 12669 13425: contig of 757 bp in length
* 13426 13525: gap of 100 bp
* 13526 14272: contig of 747 bp in length
* 14273 14372: gap of 100 bp
* 14373 15121: contig of 749 bp in length
* 15122 15221: gap of 100 bp
* 15222 15966: contig of 745 bp in length
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* 16809 16908: gap of 100 bp
* 16909 17670: contig of 762 bp in length
* 17671 17770: gap of 100 bp
* 17771 18520: contig of 750 bp in length
* 18521 18620: gap of 100 bp
* 18621 19371: contig of 751 bp in length
* 19372 19471: gap of 100 bp
* 19472 20154: contig of 683 bp in length
* 20155 20254: gap of 100 bp
* 20255 21018: contig of 764 bp in length

```

The 5' clone is M

Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/sgd-graph.cgi?c=MG7
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S. M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://genome1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MCM23.

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	pir T09939	
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Best Local Similarity 100.0%; Pred. No. 0.088; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173

Db 61644 TTATTTCAAAAAAAAAAAAAA 61620

RESULT 33

AC040952/c

LOCUS

DEFINITION Homo sapiens chromosome 17 clone -2125K20 map 17, LOW-PASS SEQUENCE SAMPLING.

AC040952

VERSION AC040952.1 GI:7534153

KEYWORDS HTG; HTGS_PHASE0.

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 85812)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone -2125K20

2 (bases 1 to 85812)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,

Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campolaviano, A., Castle, A., Choquel, Y., Colangelo, M., Collins, S.,

Collamore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Gadigan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,

Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,

Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,

Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9152

Center clone name: 2125_K_20

* NOTE: This record contains 91 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1 828: contig of 828 bp in length

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* 929 1791: contig of 863 bp in length

* 1792 1891: gap of 100 bp

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* 3640 3739: gap of 100 bp

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* 7444 8293: contig of 850 bp in length

* 8294 8393: gap of 100 bp

* 8394 9223: contig of 830 bp in length

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* 9324 10180: contig of 857 bp in length

* 10181 10280: gap of 100 bp

* 10281 11120: contig of 840 bp in length

* 11121 11220: gap of 100 bp

* 11221 12083: contig of 863 bp in length

* 12084 12183: gap of 100 bp

* 12184 13055: contig of 872 bp in length

* 13056 13155: gap of 100 bp

* 13156 14010: contig of 855 bp in length

* 14011 14110: gap of 100 bp

* 14111 14961: contig of 851 bp in length

* 14962 15061: gap of 100 bp

* 15062 15939: contig of 878 bp in length

* 15940 16039: gap of 100 bp

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* 16956 17803: contig of 848 bp in length

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* 19778 20614: contig of 837 bp in length

* 20615 20714: gap of 100 bp

* 20715 21577: contig of 863 bp in length

* 21578 21677: gap of 100 bp

* 21678 22508: contig of 831 bp in length

* 22509 22608: gap of 100 bp

* 22609 23448: contig of 840 bp in length

* 23449 23548: gap of 100 bp

* 23549 24424: contig of 876 bp in length

* 24425 24524: gap of 100 bp

* 24525 25368: contig of 844 bp in length

* 25369 25468: gap of 100 bp

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* 26338 26437: gap of 100 bp

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* 29112 29943: contig of 832 bp in length

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* 62183 63017: contig of 835 bp in length
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* 64077 64953: contig of 877 bp in length

* 64954 65053: gap of 100 bp
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Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 10593 TTATTTCAAAAAAAAAAAAAA 10569
RESULT 34
AC005646
LOCUS
DEFINITION
Drosophila melanogaster chromosome 2 clone DS00968 (D404) map
51B1-51B4 strain Y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 3
unordered pieces.
AC005646
VERSION
AC005646.6 GI:6554236
KEYWORDS
HTG; HTGS_PHASE1.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 86677)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R.,
Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B.,
Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,
Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
Sequencing of Drosophila melanogaster
Unpublished
2 (bases 1 to 86677)
Celniker, S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A.,
Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C.,
Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,
Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,
Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R.,
Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., PUNCH, E.,
Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R.,
Zier, L.L. and Kimmel, B.E.
Direct Submission
Submitted (10-SEP-1998) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Dec 10, 1999 this sequence version replaced gi:5656719.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive web site (<http://www.fruitfly.org/sequence/>) or send email
to bdg@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases. P1 library location:
8-11.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 296: contig of 296 bp in length
* 297 376: gap of unknown length
* 377 85947: contig of 85571 bp in length
* 85948 86027: gap of unknown length
* 86028 86677: contig of 650 bp in length.
* Location/Qualifiers
1. .86677
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/strain="Y: cn bw sp"
/db_xref="taxon:7227"

/db_xref="GI:7711066"
 /translation="MKKKKHYSIKFVNVDKNKYVLCSDKYIRIINYMIGLHIFRL
 QKIHVYFANQIASSPESHKYNRYTKEDLIIDGIEKWFNIDYILISEIKQNDPFS
 NDIKITVAMKMKQLLTYSINKKIDTVNASFQWASPEYIFLNIKFSHRWSSPGA
 LKVKDEEIVKKNFSSALSNDNSVTKYIVDLTLDDNIIIESETKYNFASGKVYV
 TLKKEKKIWRLLSKSEKYPNMQVWMDMEKRIHITFTVTLNLFLLSLSHRYHDSV
 QNFLKEKNNSDKLQDDIDEDEKYFDDEILREAKKSEEDYKDEEL"
 7790..7799
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 2 of
 PFC0581w"
 7830..7835
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 2 of
 PFC0581w"
 7901..7911
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 3 of
 PFC0581w"
 7941..7947
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 3 of
 PFC0581w"
 8055..8063
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 4 of
 PFC0581w"
 8107..8112
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 4 of
 PFC0581w"
 8293..8301
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 5 of
 PFC0581w"
 8369..8374
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 5 of
 PFC0581w"
 8559..8567
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 6 of
 PFC0581w"
 8642..8647
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 6 of
 PFC0581w"
 8704..8712
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 7 of
 PFC0581w"
 8813..8818
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 7 of
 PFC0581w"
 8913..8923
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 8 of
 PFC0581w"
 9007..9012
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 8 of
 PFC0581w"
 9112..9121
 /gene="PFC0581w"
 /note="potential splice acceptor sequence for exon 9 of
 PFC0581w"
 9259..9264
 /gene="PFC0581w"
 /note="potential splice donor sequence for exon 9 of
 PFC0581w"
 9361..9368
 /gene="PFC0581w"

Query Match 2.1%; Score 25; DB 3; Length 86827;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1149 ttatttcaaaaaaaaaaaaaa 1173
 |||||
 Db 34412 TTATTTCAAAAAAAAAAAAAA 34388

RESULT 36
 AC010796/c
 LOCUS AC010796 87400 bp DNA PLN 19-JAN-2001
 DEFINITION Arabidopsis thaliana chromosome 1 BAC F24J13 genomic sequence,
 complete sequence.
 ACCESSION AC010796
 VERSION AC010796.7 GI:12325034
 KEYWORDS HTG.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.
 1 (bases 1 to 87400)
 Lin.X., Kaul.S., Town.C.D., Benito.M., Creasy,T.H., Haas.B.J.,
 Wu.D., Waiiti.R., Renning.C.M., Koo.H., Fujii.C.Y., Utterback.T.R.,
 Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
 Arabidopsis thaliana chromosome 1 BAC F24J13 genomic sequence
 Unpublished
 2 (bases 1 to 87400)
 Lin.X. and Kaul.S.
 Direct Submission
 Submitted (23-SEP-1999) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, xlinetigr.org
 3 (bases 1 to 87400)
 Town.C.D. and Kaul.S.
 Direct Submission
 Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, cdtownetigr.org
 On Jan 19, 2001 this sequence version replaced gi:12280801.
 Address all correspondence to:atetigr.org

BAC clone F24J13 is from Arabidopsis thaliana chromosome 1
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of several methods: Gene
 prediction programs including Genscan+ (Chris Burge,
 http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM (Mark Borodovsky,
 http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
 of GlimmerW, see Mihaela Pertea,
 http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html, and
 GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
 mpertea@tigr.org), searches of the complete sequence against a
 peptide database and the plant EST database at TIGR
 (http://www.tigr.org/tldb/tgi.shtml). Annotated genes are named to
 indicate the level of evidence for their annotation. Genes with
 similarity to other proteins are named after the database hits.
 Genes without significant peptide similarity but with EST
 similarity are named as unknown proteins. Genes without protein
 or EST similarity, that are predicted by more than two gene
 prediction programs over most of their length are annotated as
 hypothetical proteins. Genes encoding tRNAs are predicted by
 tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
 Simple repeats are identified by repeatmasker (Arian Smit,
 http://ftp.genome.washington.edu/RM/RepeatMasker.html).

FEATURES
 Source
 1..87400
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="1"
 /clone="F24J13"
 complement(<1..>433)

mRNA

Db 10154 TTATTTCACAAAAA 10130

RESULT 37

AC007076

LOCUS

DEFINITION

AC007076 95477 bp DNA 27-APR-2000
Homo sapiens PAC clone RP4-698F7 from 7p15.1-p13, complete
sequence.

AC007076

VERSION

AC007076.3

KEYWORDS

HTG.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/OTB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-456N16, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-698F7; actual end is at base position 16254 of RP11-456N16.

The sequence RP4-698F7 contains a tandem repeat from base position 38292 to 29389. The tandem size is believed to be in agreement with PCR and digest information. The tandem area falls within band sizes of 8391 insilico, 8452 real for ecorv; and 5096 insilico, 5128 real for hindiii.

FEATURES

Location/Qualifiers	Source
1..95477	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="7"
	/map="7p15.1-p13"
	/clone="RP4-698F7"
	/clone_lib="RPI-4"
repeat_region 157..281	
	/rpt_family="MaLR"
repeat_region 730..901	
	/rpt_family="L2"
repeat_region 1596..1838	
	/rpt_family="MIR"
repeat_region 2317..2638	
	/rpt_family="Retroviral"
repeat_region 2863..3454	
	/rpt_family="Retroviral"
repeat_region 3500..3821	
	/rpt_family="Retroviral"
repeat_region 3950..4153	
	/rpt_family="Retroviral"
repeat_region 4154..4553	
	/rpt_family="Retroviral"
repeat_region 4557..5051	
	/rpt_family="L1"
repeat_region 5089..5119	
	/rpt_family="AT-rich"
repeat_region 5183..5439	
	/rpt_family="L1"
repeat_region 5450..5478	
	/rpt_family="(TTTG)n"
repeat_region 5482..5722	
	/rpt_family="Alu"
repeat_region 5744..6052	
	/rpt_family="L1"
repeat_region 6307..6433	
	/rpt_family="L1"
repeat_region 6969..7546	
	/rpt_family="Retroviral"
repeat_region 9216..9463	
	/rpt_family="L1"
STS 11308..11484	
	/db_xref="GI:1232262"
repeat_region 11392..11431	
	/rpt_family="(CA)n"

STS

repeat_region

AC007076 95477 bp DNA 27-APR-2000
Homo sapiens PAC clone RP4-698F7 from 7p15.1-p13, complete
sequence.
AC007076
AC007076.3 GI:6604547
HTG.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 95477)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
2 (bases 1 to 95477)
Ozersky, P., Kalicki, J. and Smith, R.
The sequence of Homo sapiens PAC clone RP4-698F7
Unpublished
3 (bases 1 to 95477)
Direct Submission
Waterston, R.H.
Submitted (13-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 95477)
Waterston, R.H.
Direct Submission
Submitted (19-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 95477)
Waterston, R.H.
Direct Submission
Submitted (21-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 95477)
Waterston, R.
Direct Submission
Submitted (27-APR-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 20, 1999 this sequence version replaced gi:5001547.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: saplens@wustl.wustl.edu
----- Summary Statistics

Center project name: H_DJ0698F07

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping

```

repeat_region 12041..12131
/rpt_family="MERL_type"
repeat_region 12186..12314
/rpt_family="MaLR"
repeat_region 12315..12801
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repeat_region 12802..13106
/rpt_family="MaLR"
repeat_region 13918..13968
/rpt_family="L1"
repeat_region 13971..13997
/rpt_family="(TTTC)n"
repeat_region 13998..14285
/rpt_family="Alu"
repeat_region 14286..14685
/rpt_family="L1"
repeat_region 17206..17506
/rpt_family="Alu"
repeat_region 18905..19246
/rpt_family="L1"
repeat_region 20906..21274
/rpt_family="MaLR"
repeat_region 21432..21452
/rpt_family="AT_rich"
repeat_region 24864..24892
/rpt_family="(T)n"
misc_feature 24888..25144
/notes="similar to EST AW085212 (NID:g6040364) xe07c06.x1"
repeat_region 25373..26235
/rpt_family="L1"
repeat_region 26225..26700
/rpt_family="L1"
repeat_region 26732..26844
/rpt_family="Alu"
repeat_region 27061..27096
/rpt_family="AT_rich"
repeat_region 27262..27311
/rpt_family="Alu"
repeat_region 27313..27470
/rpt_family="(GAAA)n"
repeat_region 27530..27699
/rpt_family="Retroviral"
repeat_region 27902..27992
/rpt_family="MERL_type"
repeat_region 27991..28081
/rpt_family="MERL_type"
repeat_region 28097..28225
/rpt_family="L1"
repeat_region 28284..28442
/rpt_family="MERL_type"
repeat_region 28311..28464
/rpt_family="MERL_type"
STS complement(29279..29700)
/db_xref="GI:5223519"
repeat_region 29862..29963
/rpt_family="MIR"
repeat_region 31105..31222
/rpt_family="L1"
repeat_region 31242..31553

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Query Match 2.1%; Score 25; DB 9; Length 95477;
 Best Local Similarity 100.0%; Pred. No. 0.086;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaa 1173
 |||
 Db 17482 TTATTTCACAAAAA 17506

RESULT 38
 AL356791 101157 bp DNA PRI 12-JAN-2001
 LOCUS Human DNA sequence from clone RP11-8013 on chromosome 9 Contains
 DEFINITION

GSSs and STSs, complete sequence.

```

ACCESSION AL356791
VERSION AL356791.9 GI:11877989
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 101157)
AUTHORS Barker, D.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Dec 17, 2000 this sequence version replaced gi:11863404.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-8013 is from the library RPCI-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-8013 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-8013 is at 101157 in this
sequence. The true right end of clone RP11-47769 is at 100 in this
sequence.
FEATURES
Source Location/Qualifiers
1..101157
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-8013"
/clone_lib="RPCI-11.1"
256..393
/notes="L2 repeat: matches 2602..2746 of consensus"
complement(581..1430)
/notes="match: STS: Em:G62385"
complement(791..1461)
/notes="match: GSS: Em:AQ480671"
complement(921..1451)
/notes="match: GSS: Em:AQ570464"
complement(1069..1461)
/notes="match: GSS: Em:AQ664824"
complement(1098..1382)
/notes="match: GSS: Em:AQ594692"
1134..1177
/notes="MIR repeat: matches 97..139 of consensus"
complement(1967..2460)
/notes="match: GSS: Em:AQ412192"
2191..2450
/notes="AluX repeat: matches 1..260 of consensus"
complement(2692..3207)
/notes="match: GSS: Em:A2519746"
2873..2886
repeat_region
misc_feature
misc_feature
misc_feature
misc_feature
misc_feature
repeat_region
misc_feature
repeat_region
misc_feature
repeat_region

```

```
repeat_region /note="L1MA7 repeat: matches 6154. .6166 of consensus"
3071. .3759
repeat_region /note="L2 repeat: matches 1984. .2750 of consensus"
4348. .4732
repeat_region /note="MIT2A repeat: matches 8. .397 of consensus"
4735. .4758
repeat_region /note="6 copies 4 mer ctct 100% conserved"
4763. .4862
repeat_region /note="HERVL repeat: matches 139. .238 of consensus"
4863. .5630
repeat_region /note="192 copies 4 mer atat 66% conserved"
5630. .5775
repeat_region /note="73 copies 2 mer at 80% conserved"
5631. .5822
repeat_region /note="48 copies 4 mer tata 73% conserved"
5823. .5861
repeat_region /note="MIT2A repeat: matches 407. .449 of consensus"
5862. .11474
repeat_region /note="HERVL repeat: matches 1. .5654 of consensus"
11475. .11780
repeat_region /note="MIT2B repeat: matches 1. .313 of consensus"
11797. .11834
repeat_region /note="MIT2A repeat: matches 416. .453 of consensus"
11876. .11929
repeat_region /note="MIT1F repeat: matches 76. .127 of consensus"
12146. .12201
repeat_region /note="L2 repeat: matches 2650. .2705 of consensus"
14674. .14741
misc_feature /note="34 copies 2 mer aa 73% conserved"
16776. .17286
repeat_region /note="match: GSS: Em:AQ150535"
16939. .17230
repeat_region /note="L1PA9 repeat: matches 5853. .6161 of consensus"
17319. .17439
repeat_region /note="FIAM_C repeat: matches 1. .121 of consensus"
18321. .18476
misc_feature /note="MIR repeat: matches 47. .204 of consensus"
18480. .18673
misc_feature /note="match: GSS: Em:AQ070516"
complement(19222. .19612)
repeat_region /note="match: GSS: Em:AQ535364"
20239. .20284
repeat_region /note="L2 repeat: matches 2460. .2486 of consensus"
20265. .20565
repeat_region /note="AluY repeat: matches 1. .302 of consensus"
20566. .20767
repeat_region /note="L2 repeat: matches 2486. .2673 of consensus"
20770. .20841
repeat_region /note="L2 repeat: matches 2670. .2743 of consensus"
21026. .22427
repeat_region /note="L2 repeat: matches 857. .2417 of consensus"
22439. .22500
repeat_region /note="L2 repeat: matches 2687. .2750 of consensus"
22894. .23016
misc_feature /note="3 copies 41 mer 77% conserved"
23116. .23798
misc_feature /note="match: GSS: Em:B82580"
23165. .23625
misc_feature /note="match: GSS: Em:AQ896235"
complement(23562. .24064)
misc_feature /note="match: GSS: Em:AQ555111"
complement(23656. .24064)
misc_feature /note="match: GSS: Em:AQ299045"
complement(24055. .24524)
repeat_region /note="match: GSS: Em:AQ720866"
24096. .24405
repeat_region /note="AluY repeat: matches 3. .302 of consensus"
24948. .25184
repeat_region /note="MIR repeat: matches 10. .262 of consensus"
25350. .25501
repeat_region /note="FRAM repeat: matches 1. .156 of consensus"
26263. .26296
repeat_region /note="17 copies 2 mer aa 88% conserved"
```

```
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/note="MIR repeat: matches 28. .111 of consensus"
26811. .27106
repeat_region /note="AluX repeat: matches 1. .296 of consensus"
28376. .28568
repeat_region /note="MLT1I repeat: matches 211. .403 of consensus"
31895. .32057
repeat_region /note="MERSB repeat: matches 1. .174 of consensus"
32239. .32366
repeat_region /note="MER7A repeat: matches 1. .126 of consensus"
32378. .32614
repeat_region /note="MER33 repeat: matches 52. .296 of consensus"
32977. .33137
repeat_region /note="MIR repeat: matches 2. .163 of consensus"
33249. .33488
repeat_region /note="L2 repeat: matches 2434. .2710 of consensus"
34725. .35062
repeat_region /note="MER7A repeat: matches 1. .346 of consensus"
35513. .35598
repeat_region /note="MIR repeat: matches 117. .197 of consensus"
35788. .35956
repeat_region /note="MIR repeat: matches 37. .215 of consensus"
37248. .37374
misc_feature /note="L2 repeat: matches 2574. .2688 of consensus"
complement(37683. .38110)
repeat_region /note="match: GSS: Em:AQ764674"
38347. .38630
repeat_region /note="AluY repeat: matches 1. .298 of consensus"
40121. .40238
repeat_region /note="MLT1J repeat: matches 1. .120 of consensus"
40884. .41367
repeat_region /note="MLT2CB repeat: matches 1. .501 of consensus"
43159. .43364
repeat_region /note="L2 repeat: matches 2307. .2507 of consensus"
43438. .43655
repeat_region /note="MER20 repeat: matches 1. .218 of consensus"
44967. .45042
repeat_region /note="L2 repeat: matches 2607. .2691 of consensus"
45072. .45380
misc_feature /note="AluSq repeat: matches 1. .308 of consensus"
45200. .45641
misc_feature /note="match: GSS: Em:AQ461292"
complement(46363. .46835)
repeat_region /note="match: GSS: Em:AQ407114"
46653. .46992
misc_feature /note="MER61A repeat: matches 4. .354 of consensus"
46837. .47247
repeat_region /note="match: GSS: Em:AQ459068"
48337. .48645
repeat_region /note="AluJo repeat: matches 2. .310 of consensus"
51443. .51565
repeat_region /note="L2 repeat: matches 2103. .2228 of consensus"
```

Query Match

Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173

DB 83293 TTATTTCACAAAAAAAAAAAAAAAAA 83317

RESULT 39

AC008623/c AC008623 128266 bp DNA PRI 07-NOV-2000

LOCUS Homo sapiens chromosome 19 clone CTB-14D10, complete sequence.

DEFINITION AC008623

ACCESSION AC008623.4 GI:11119446

VERSION HTG.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```
repeat_region /rpt_family="Alu" complement(46346..46611)
repeat_region /rpt_family="Alu" 48448..48568
repeat_region /rpt_family="Alu" 51621..52057
repeat_region /rpt_family="Alu" complement(52840..53083)
repeat_region /rpt_family="Alu" 55877..56194
repeat_region /rpt_family="L1" complement(56726..57195)
repeat_region /rpt_family="MER4" 57231..57481
repeat_region /rpt_family="Alu" complement(58018..58314)
repeat_region /rpt_family="Alu" 60304..60417
repeat_region /rpt_family="MER20" complement(66136..66391)
repeat_region /rpt_family="Alu" complement(67813..67896)
repeat_region /rpt_family="MER42" 70956..71184
repeat_region /rpt_family="Alu" complement(71638..73604)
repeat_region /rpt_family="L1" 72541..72866
repeat_region /rpt_family="THE1" complement(75532..75805)
repeat_region /rpt_family="Alu" 76188..76305
repeat_region /rpt_family="Alu" complement(79990..80123)
repeat_region /rpt_family="Tigger1" complement(80125..80489)
repeat_region /rpt_family="THE1" complement(80489..82456)
repeat_region /rpt_family="Tigger1" 80722..80980
repeat_region /rpt_family="Alu" 82077..82193
repeat_region /rpt_family="Alu" complement(82507..83376)
repeat_region /rpt_family="LTR12" complement(83986..84246)
repeat_region /rpt_family="Tigger1" 86796..87084
repeat_region /rpt_family="Alu" 91321..91639
repeat_region /rpt_family="Alu" complement(93060..93336)
repeat_region /rpt_family="Alu" complement(94383..94940)
repeat_region /rpt_family="Alu" 95168..95729
repeat_region /rpt_family="LTR12" 96121..96380
repeat_region /rpt_family="Alu" 96589..96930
repeat_region /rpt_family="L1" 97057..97320
repeat_region /rpt_family="MER33" 98665..100457
repeat_region /rpt_family="L1" 101098..101370
repeat_region /rpt_family="Alu" 102272..102495
repeat_region /rpt_family="Alu" 104468..104861
repeat_region /rpt_family="Tigger2" 105161..105441
repeat_region /rpt_family="MER2" 105161..105441
```

```
repeat_region 105920..106146 /rpt_family="Alu"
repeat_region 106424..106651 /rpt_family="Alu"
repeat_region 107088..107514 /rpt_family="MER4"
repeat_region complement(109038..109314) /rpt_family="Alu"
repeat_region 109449..109623 /rpt_family="MER4"
repeat_region 109893..110067 /rpt_family="MER4"
repeat_region complement(110667..110953) /rpt_family="Alu"
repeat_region 111038..111200 /rpt_family="MER4"
repeat_region 111282..111680 /rpt_family="MER4"
repeat_region 112620..112907 /rpt_family="Alu"
repeat_region 112951..113027 /rpt_family="Alu"
repeat_region 113435..114149 /rpt_family="LTR8"
repeat_region complement(114239..114392)
```

Query Match 2.1%; Score 25; DB 2; Length 131541;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttattcaaaaaaaaaaaaaa 1173
|||||
Db 49282 TTATTCAAAAAAAAAAAAA 49258

RESULT 41

AL445071
LOCUS AL445071 135056 bp DNA PRI 19-JAN-2001
DEFINITION Human DNA sequence from clone RP11-460H18 on chromosome 10,
complete sequence.
ACCESSION AL445071 GI:12329452
VERSION AL445071.14
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 135056)
AUTHORS Howden, P.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 21, 2001 this sequence version replaced gi:12192066.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr10>
 RP11-460H18 is from the library RPCI-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-460H18 it may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true right end of clone RP11-460H18 is at 135056 in this
 sequence. The true left end of clone RP11-166N17 is at 73000 in
 this sequence.

FEATURES

source	Location/Qualifiers
	1. 135056
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="10"
	/clone="RP11-460H18"
	/clone_lib="RPCI-11.2"
	2. 101
repeat_region	/note="BUR1 repeat: matches 6167. .6266 of consensus"
repeat_region	103. .252
repeat_region	/note="LTP23 repeat: matches 205. .342 of consensus"
repeat_region	372. .513
repeat_region	/note="MIR repeat: matches 110. .252 of consensus"
repeat_region	536. .668
repeat_region	/note="FLAM_C repeat: matches 1. .133 of consensus"
repeat_region	726. .866
repeat_region	/note="MER4A2 repeat: matches 1. .152 of consensus"
repeat_region	867. .955
repeat_region	/note="MER4A repeat: matches 367. .451 of consensus"
repeat_region	959. .1347
repeat_region	/note="LTP7 repeat: matches 1. .450 of consensus"
repeat_region	1348. .1906
repeat_region	/note="HRRVH repeat: matches 7157. .7713 of consensus"
repeat_region	1900. .2160
repeat_region	/note="HRRVH repeat: matches 5756. .6016 of consensus"
repeat_region	2151. .3416
repeat_region	/note="HRRVH repeat: matches 3357. .4719 of consensus"
repeat_region	3425. .5156
repeat_region	/note="HRRVH repeat: matches 1124. .2814 of consensus"
repeat_region	5147. .5723
repeat_region	/note="HRRVH repeat: matches 1. .576 of consensus"
repeat_region	5724. .6112
repeat_region	/note="LTP7 repeat: matches 1. .450 of consensus"
repeat_region	6113. .6301
repeat_region	/note="MER4A2 repeat: matches 293. .486 of consensus"
repeat_region	7100. .7412
repeat_region	/note="AluJb repeat: matches 1. .292 of consensus"
repeat_region	7463. .8072
repeat_region	/note="MER4B repeat: matches 1. .609 of consensus"
repeat_region	8166. .8258
repeat_region	/note="L2 repeat: matches 2596. .2698 of consensus"
repeat_region	9115. .9402
repeat_region	/note="AluX repeat: matches 11. .312 of consensus"
repeat_region	9413. .9673
repeat_region	/note="AluJo repeat: matches 3. .300 of consensus"
repeat_region	9679. .9977
repeat_region	/note="AluJo repeat: matches 6. .305 of consensus"
repeat_region	10415. .10591
repeat_region	/note="MIR repeat: matches 21. .192 of consensus"
repeat_region	10714. .10799
repeat_region	/note="L2 repeat: matches 2627. .2710 of consensus"
repeat_region	10848. .10931
repeat_region	/note="MER76 repeat: matches 597. .688 of consensus"
repeat_region	10948. .11165
repeat_region	/note="AluJo repeat: matches 1. .230 of consensus"
repeat_region	11176. .11482
repeat_region	/note="AluSp repeat: matches 1. .308 of consensus"
repeat_region	11579. .11740
repeat_region	/note="AluJo repeat: matches 1. .152 of consensus"
repeat_region	11797. .12095
repeat_region	/note="AluJo repeat: matches 1. .297 of consensus"
repeat_region	12098. .12674

/note="MER76 repeat: matches 2. .613 of consensus"	12743. .13056
/note="AluJo repeat: matches 5. .311 of consensus"	13346. .13429
/note="MLTIE repeat: matches 478. .560 of consensus"	13736. .13780
/note="MER53 repeat: matches 2. .41 of consensus"	13781. .14080
/note="AluX repeat: matches 1. .302 of consensus"	14081. .14161
/note="MER53 repeat: matches 41. .140 of consensus"	14417. .14624
/note="LTPB3 repeat: matches 5942. .6149 of consensus"	14640. .14935
/note="AluX repeat: matches 1. .303 of consensus"	14942. .15476
/note="LTPB3 repeat: matches 5612. .6150 of consensus"	15625. .15827
/note="AluJo repeat: matches 25. .187 of consensus"	15828. .16136
/note="AluX repeat: matches 1. .310 of consensus"	16137. .16236
/note="AluJo repeat: matches 187. .296 of consensus"	17416. .17433
/note="FLAM_A repeat: matches 125. .142 of consensus"	17434. .17769
/note="AluYb8 repeat: matches 1. .310 of consensus"	17770. .17895
/note="FLAM_A repeat: matches 1. .125 of consensus"	18500. .18776
/note="AluYb repeat: matches 9. .306 of consensus"	18842. .19085
/note="LMB6 repeat: matches 5684. .5928 of consensus"	19606. .19906
/note="AluX repeat: matches 1. .304 of consensus"	20006. .20151
/note="LMBD3 repeat: matches 7590. .7738 of consensus"	20152. .20193
/note="21 copies 2 mer gt 83% conserved"	20283. .21332
/note="LMBD repeat: matches 1277. .2272 of consensus"	21333. .21606
/note="AluJo repeat: matches 1. .270 of consensus"	21607. .21617
/note="LMBD repeat: matches 1268. .1277 of consensus"	21618. .21910
/note="AluX repeat: matches 1. .293 of consensus"	21911. .22502
/note="LMBD repeat: matches -17. .1268 of consensus"	22961. .23009
/note="L2 repeat: matches 2441. .2489 of consensus"	23523. .23614
/note="L2 repeat: matches 789. .875 of consensus"	23624. .23923
/note="AluJo repeat: matches 9. .308 of consensus"	23926. .24235
/note="AluX repeat: matches 1. .310 of consensus"	24456. .24765
/note="AluJo repeat: matches 1. .288 of consensus"	24774. .25086
/note="AluX repeat: matches 1. .309 of consensus"	25385. .25683
/note="AluX repeat: matches 1. .295 of consensus"	26038. .26339
/note="AluX repeat: matches 1. .310 of consensus"	26760. .27068
/note="L2 repeat: matches 2420. .2731 of consensus"	27069. .27359
/note="AluX repeat: matches 1. .290 of consensus"	27363. .27665
/note="AluX repeat: matches 1. .303 of consensus"	27666. .27685
/note="L2 repeat: matches 2731. .2749 of consensus"	

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repeat_region 28514..28801
/notes="AluJo repeat: matches 1. .290 of consensus"
repeat_region 29518..29613
/notes="48 copies 2 mer ac 76% conserved"
repeat_region 29675..29946
/notes="AluX repeat: matches 3. .274 of consensus"
repeat_region 30945..31083
/notes="FLAM_A repeat: matches 4. .133 of consensus"
repeat_region 31087..31396
/notes="AluX repeat: matches 3. .312 of consensus"
repeat_region 31409..31701
/notes="AluX repeat: matches 1. .295 of consensus"
repeat_region 31756..32073
/notes="AluX repeat: matches 1. .312 of consensus"
repeat_region 32361..32598
/notes="LNR33 repeat: matches 22. .251 of consensus"
repeat_region 32658..32773
/notes="MER5B repeat: matches 56. .172 of consensus"

Query Match 2.1%; Score 25; DB 9; Length 135056;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttattccaaaaaataaaaaaa 1173
|||||
Db 92127 TTATTTCAAAAAATAAAAAA 92151

RESULT 42
AP003266 142239 bp DNA 18-JUL-2001
LOCUS Oryza sativa genomic DNA, chromosome 1, PAC clone: P0492G09,
DEFINITION complete sequence.
ACCESSION AP003266
VERSION AP003266.2 GI:14861127
KEYWORDS HTG.
SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone: P0492G09.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 142239)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0492G09
JOURNAL Published Only in Database (2001) In press
REFERENCE 2 (bases 1 to 142239)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
JOURNAL Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7469)
COMMENT On Jul 17, 2001 this sequence version replaced gi:13027295.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
FEATURES
source
1..142239
/organism="Oryza sativa"
/db_xref="taxon:4530"
/chromosome="1"
/clone="P0492G09"

BASE COUNT 41829 a 30451 c 29772 g 40187 t
ORIGIN

Query Match 2.1%; Score 25; DB 8; Length 142239;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 261 gccaggagacgattccaggatgctg 285
|||||

```

Db 91132 GCCAAGGAGCAGTCAGAGTGCG 91156

RESULT 43

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AC013763 144075 bp DNA HTG 13-JUL-2000
LOCUS Homo sapiens clone RP11-2J14, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC013763
ACCESSION AC013763.3 GI:9119888
VERSION HTG; HTGS_PHASE0.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 144075)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-2J14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 144075)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Doneilan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gaidyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye.W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6492536.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2541
Center clone name: 2_J_14
-----
* NOTE: This record contains 147 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 906: contig of 906 bp in length
* 907 1006: gap of 100 bp
* 1007 1908: contig of 902 bp in length
* 1909 2008: gap of 100 bp
* 2009 2920: contig of 912 bp in length
* 2921 3020: gap of 100 bp
* 3021 3912: contig of 892 bp in length
* 3913 4012: gap of 100 bp
* 4013 4902: contig of 890 bp in length
* 4903 5002: gap of 100 bp
* 5003 5944: contig of 942 bp in length
* 5945 6044: gap of 100 bp
* 6045 6945: contig of 901 bp in length

```

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* 6946 7045: gap of 100 bp
* 7046 7929: contig of 884 bp in length
* 7930 8029: gap of 100 bp
* 8030 8945: contig of 916 bp in length
* 8946 9045: gap of 100 bp
* 9046 9947: contig of 902 bp in length
* 9948 10047: gap of 100 bp
* 10048 10962: contig of 915 bp in length
* 10963 11062: gap of 100 bp
* 11063 11963: contig of 901 bp in length
* 11964 12063: gap of 100 bp
* 12064 12974: contig of 911 bp in length
* 12975 13074: gap of 100 bp
* 13075 13990: contig of 916 bp in length
* 13991 14090: gap of 100 bp
* 14091 14956: contig of 866 bp in length
* 14957 15056: gap of 100 bp
* 15057 15925: contig of 869 bp in length
* 15926 16025: gap of 100 bp
* 16026 16936: contig of 911 bp in length
* 16937 17036: gap of 100 bp
* 17037 17958: contig of 922 bp in length
* 17959 18058: gap of 100 bp
* 18059 18959: contig of 901 bp in length
* 18960 19059: gap of 100 bp
* 19060 19957: contig of 898 bp in length
* 19958 20057: gap of 100 bp
* 20058 20951: contig of 894 bp in length
* 20952 21051: gap of 100 bp
* 21052 21931: contig of 880 bp in length
* 21932 22031: gap of 100 bp
* 22032 22921: contig of 890 bp in length
* 22922 23021: gap of 100 bp
* 23022 23906: contig of 885 bp in length
* 23907 24006: gap of 100 bp
* 24007 24889: contig of 883 bp in length
* 24890 24989: gap of 100 bp
* 24990 25882: contig of 893 bp in length
* 25883 25982: gap of 100 bp
* 25983 26881: contig of 899 bp in length
* 26882 26981: gap of 100 bp
* 26982 27892: contig of 911 bp in length
* 27893 27992: gap of 100 bp
* 27993 28908: contig of 916 bp in length
* 28909 29008: gap of 100 bp
* 29009 29860: contig of 852 bp in length
* 29861 29960: gap of 100 bp
* 29961 30853: contig of 893 bp in length
* 30854 30953: gap of 100 bp
* 30954 31868: contig of 915 bp in length
* 31869 31968: gap of 100 bp
* 31969 32859: contig of 891 bp in length
* 32860 32959: gap of 100 bp
* 32960 33849: contig of 890 bp in length
* 33850 33949: gap of 100 bp
* 33950 34823: contig of 874 bp in length
* 34824 34923: gap of 100 bp
* 34924 35803: contig of 880 bp in length
* 35804 35903: gap of 100 bp
* 35904 36787: contig of 884 bp in length
* 36788 36887: gap of 100 bp
* 36888 37761: contig of 874 bp in length
* 37762 37861: gap of 100 bp
* 37862 38769: contig of 908 bp in length
* 38770 38869: gap of 100 bp
* 38870 39774: contig of 905 bp in length
* 39775 39874: gap of 100 bp
* 39875 40761: contig of 887 bp in length
* 40762 40861: gap of 100 bp
* 40862 41777: contig of 916 bp in length
* 41778 41877: gap of 100 bp
* 41878 42788: contig of 911 bp in length
* 42789 42888: gap of 100 bp

```

```

* 42889 43774: contig of 886 bp in length
* 43775 43874: gap of 100 bp
* 43875 44776: contig of 902 bp in length
* 44777 44876: gap of 100 bp
* 44877 45738: contig of 862 bp in length
* 45739 45838: gap of 100 bp
* 45839 46717: contig of 879 bp in length
* 46718 46817: gap of 100 bp
* 46818 47723: contig of 906 bp in length
* 47724 47823: gap of 100 bp
* 47824 48717: contig of 894 bp in length
* 48718 48817: gap of 100 bp
* 48818 49736: contig of 919 bp in length
* 49737 49836: gap of 100 bp
* 49837 50744: contig of 908 bp in length
* 50745 50844: gap of 100 bp
* 50845 51751: contig of 907 bp in length
* 51752 51851: gap of 100 bp
* 51852 52738: contig of 887 bp in length
* 52739 52838: gap of 100 bp
* 52839 53752: contig of 914 bp in length
* 53753 53852: gap of 100 bp
* 53853 54749: contig of 897 bp in length
* 54750 54849: gap of 100 bp
* 54850 55747: contig of 898 bp in length
* 55748 55847: gap of 100 bp
* 55848 56755: contig of 908 bp in length
* 56756 56855: gap of 100 bp
* 56856 57738: contig of 883 bp in length
* 57739 57838: gap of 100 bp
* 57839 58743: contig of 905 bp in length
* 58744 58843: gap of 100 bp
* 58844 59758: contig of 915 bp in length
* 59759 59858: gap of 100 bp
* 59859 60758: contig of 900 bp in length
* 60759 60858: gap of 100 bp
* 60859 61748: contig of 890 bp in length
* 61749 61848: gap of 100 bp
* 61849 62731: contig of 883 bp in length
* 62732 62831: gap of 100 bp
* 62832 63750: contig of 919 bp in length
* 63751 63850: gap of 100 bp
* 63851 64725: contig of 875 bp in length
* 64726 64825: gap of 100 bp
* 64826 65738: contig of 913 bp in length
* 65739 65838: gap of 100 bp
* 65839 66734: contig of 896 bp in length
* 66735 66834: gap of 100 bp
* 66835 67729: contig of 895 bp in length
* 67730 67829: gap of 100 bp
* 67830 68709: contig of 880 bp in length
* 68710 68809: gap of 100 bp
* 68810 69695: contig of 886 bp in length
* 69696 69795: gap of 100 bp
* 69796 70681: contig of 886 bp in length
* 70682 70781: gap of 100 bp
* 70782 71663: contig of 882 bp in length
* 71664 71763: gap of 100 bp
* 71764 72649: contig of 886 bp in length

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Query Match 2.1%; Score 25; DB 2; Length 144075;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1149 ttatttcaaaaaaaaaaaaaaa 1173
 |||||
 Db 113280 TTATTCAAAAAAAAAAAAAA 113304

RESULT 44
 AC023459/c
 LOCUS
 DEFINITION Homo sapiens chromosome 20 clone RP11-778f12 map 20, WORKING DRAFT

HTG
 09-MAR-2000

Fri Dec 28 09:12:30 2001

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Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1149 ttatttcaaaaaaaaaaaaaaa 1173
Db 5827 TTATTTCAAAAAAAAAAAAAAAAAA 5803

RESULT 45
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DEFINITION Homo sapiens clone RP11-395C3, WORKING DRAFT SEQUENCE, 26 unordered
pieces.
ACCESSION AC023196
VERSION AC023196.2 GI:7139743
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE

1 (bases 1 to 147246)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Homo sapiens, clone RP11-395C3
 Unpublished
 2 (bases 1 to 147246)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
 Boguslavsky,L., Bouknight,B., Brown,A., Burkett,G., Castle,A.,
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 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
 Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
 McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
 Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
 Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu,X., Wyman,D., Ye,W.J.,
 Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 1, 2000 this sequence version replaced gi:6957785.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: W18R
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L5884
 Center clone name: 395_C_3
 ----- Summary Statistics
 Sequencing vector: M13: M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 135851 bases at least Q40
 Consensus quality: 141251 bases at least Q30
 Consensus quality: 143252 bases at least Q20
 Insert size: 155000; agarose-fp
 Insert size: 144746; sum-of-contigs
 Quality coverage: 4.3 in Q20 bases; agarose-fp
 Quality coverage: 4.6 in Q20 bases; sum-of-contigs

TITLE

JOURNAL

COMMENT

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 26 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved. 1212: contig of 1212 bp in length
 * 1213 1312: gap of 100 bp
 * 1313 2624: contig of 1312 bp in length
 * 2625 2724: gap of 100 bp
 * 2725 4183: contig of 1459 bp in length
 * 4184 4283: gap of 100 bp
 * 4284 5963: contig of 1680 bp in length
 * 5964 6063: gap of 100 bp
 * 6064 7954: contig of 1891 bp in length
 * 7955 8054: gap of 100 bp
 * 8055 9299: contig of 1245 bp in length
 * 9300 9399: gap of 100 bp
 * 9400 11758: contig of 2359 bp in length
 * 11759 11858: gap of 100 bp
 * 11859 14613: contig of 2755 bp in length

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glnde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hegos, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, I., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Soudnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Triggilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (31-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 31, 2001 this sequence version replaced g1:14150912.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L1085

Center clone name: 44_K_6

FEATURES

source Location/Qualifiers

1. 149008
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/db_xref="taxon:9606"
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/clone_lib="RPC1-11 Human Male BAC"

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repeat_region

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repeat_region

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repeat_region

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unsure

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* 2721 3530: contig of 810 bp in length
* 3531 3630: gap of 100 bp
* 3631 4455: contig of 825 bp in length
* 4456 4555: gap of 100 bp
* 4556 5366: contig of 811 bp in length
* 5367 5466: gap of 100 bp
* 5467 6291: contig of 825 bp in length
* 6292 6391: gap of 100 bp
* 6392 7209: contig of 818 bp in length
* 7210 7309: gap of 100 bp
* 7310 8125: contig of 816 bp in length
* 8126 8225: gap of 100 bp
* 8226 9022: contig of 797 bp in length
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* 9123 9915: contig of 793 bp in length
* 9916 10015: gap of 100 bp
* 10016 10821: contig of 806 bp in length
* 10822 10921: gap of 100 bp
* 10922 11753: contig of 832 bp in length
* 11754 11853: gap of 100 bp
* 11854 12691: contig of 838 bp in length
* 12692 12791: gap of 100 bp
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* 13713 14525: contig of 813 bp in length
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* 15452 15531: gap of 100 bp
* 15532 16371: contig of 820 bp in length
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* 60962 61769: contig of 808 bp in length
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Query Match 2.18; Score 25; DB 2; Length 153846;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173

DB 55076 TTATTTCAAAAAAAAAAAAAA 55052

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RESULT 49
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SV AC073662.2
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XX 06-JUL-2000 (Rel. 64, Created)
DT 24-JUL-2000 (Rel. 64, Last updated, Version 2)
DT
XX
DE Homo sapiens chromosome 4 clone RP11-59815 map 4, WORKING DRAFT SEQUENCE,
DE 23 unordered pieces.
XX
XX HTG; HTGS_DRAFT; HTGS_PHASE1.
XX
XX Homo sapiens (human)
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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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XX [1]
RP 1-156847
RA Birren B., Linton L., Nusbaum C., Lander E.;
RA "Homo sapiens chromosome 4, clone RP11-59815";
RL Unpublished.
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RA O'Donnell P., O'Neill D., Ollivar T.M., Oliver J., Peterson K., Pierre N.,
RA Pisaní C., Pollara V., Raymond C., Riley R., Rogov P., Rothman D., Roy A.,
RA Santos R., Schauer S., Severy P., Spencer B., Stange-Thomann N.,
RA Stojanovic N., Subramanian A., Talamas J., Tesfaye S., Theodore J.,
RA Tirrell A., Travers M., Trigilio J., Vassiliev H., Viel R., Vo A.,
RA Wilson B., Wu X., Wyman D., Ye W.J., Young G., Zainoun J., Zimmer A.,
RA Zody M.;
RT
RL Submitted (28-JUN-2000) to the EMBL/GenBank/DBJ databases.
RL Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
RL Cambridge, MA 02141, USA
XX
XX On Jul 22, 2000 this sequence version replaced gi:8783350.
CC All repeats were identified using RepeatMasker:
CC Smit, A.F.A. & Green, P. (1996-1997)
CC http://ftp.genome.washington.edu/RM/RepeatMasker.html
CC ----- Genome Center
CC Center: Whitehead Institute/ MIT Center for Genome Research
CC Center code: WIBR
CC Web site: http://www-seq.wi.mit.edu
CC Contact: sequence_submissions@genome.wi.mit.edu
CC ----- Project Information
CC Center project name: I9561
CC Center clone name: 598_I_5
CC ----- Summary Statistics
CC Sequencing vector: M13; M77815; 100% of reads
CC Chemistry: Dye-terminator Big Dye; 100% of reads
CC Assembly program: Phrap; version 0.960731
CC Consensus quality: 144955 bases at least Q40
CC Consensus quality: 150878 bases at least Q30
CC Consensus quality: 153325 bases at least Q20
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Insert size: 157000; agarose-fp
Insert size: 15647; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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* 1210 1309: gap of 100 bp
* 1310 3241: contig of 1932 bp in length
* 3242 3341: gap of 100 bp
* 3342 4783: contig of 1442 bp in length
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* 4884 6670: contig of 1787 bp in length
* 6671 6770: gap of 100 bp
* 6771 9644: contig of 2874 bp in length
* 9645 9744: gap of 100 bp
* 9745 11584: contig of 1840 bp in length
* 11585 11684: gap of 100 bp
* 11685 14217: contig of 2533 bp in length
* 14218 14317: gap of 100 bp
* 14318 16794: contig of 2477 bp in length
* 16795 16894: gap of 100 bp
* 16895 19966: contig of 3072 bp in length
* 19967 20066: gap of 100 bp
* 20067 22959: contig of 2893 bp in length
* 22960 23059: gap of 100 bp
* 23060 26760: contig of 3701 bp in length
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* 26861 31471: contig of 4611 bp in length
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* 31572 37969: contig of 6298 bp in length
* 37970 37969: gap of 100 bp
* 37970 43507: contig of 5538 bp in length
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* 43608 51571: contig of 7964 bp in length
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* 59635 59734: gap of 100 bp
* 59735 69964: contig of 10230 bp in length
* 69965 70064: gap of 100 bp
* 70065 80575: contig of 10511 bp in length
* 80576 80675: gap of 100 bp
* 80676 93171: contig of 12496 bp in length
* 93172 93271: gap of 100 bp
* 93272 105534: contig of 12263 bp in length
* 105535 105634: gap of 100 bp
* 105635 120586: contig of 14952 bp in length
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* 120687 137862: contig of 17176 bp in length
* 137863 137962: gap of 100 bp
* 137963 156847: contig of 18885 bp in length.

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 80780 TTATTTCAAAAAAAAAAAAAAAAA 80756

RESULT 50
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SEQUENCE, 2 ordered pieces.
ACCESSION AC083838
VERSION AC083838
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157525)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 8, clone RP11-42L4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 157525)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavskiy,L.,

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TITLE
JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Center project name: L11292

Center clone name: 42_L4

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 156921 bases at least Q40

Consensus quality: 157145 bases at least Q30

Consensus quality: 157310 bases at least Q20

Insert size: 157000; agarose-fp

Insert size: 157425; sum-of-contigs

Quality coverage: 14.1 in Q20 bases; agarose-fp

Quality coverage: 14.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
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 * 77303 157525: contig of 80223 bp in length.
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FEATURES
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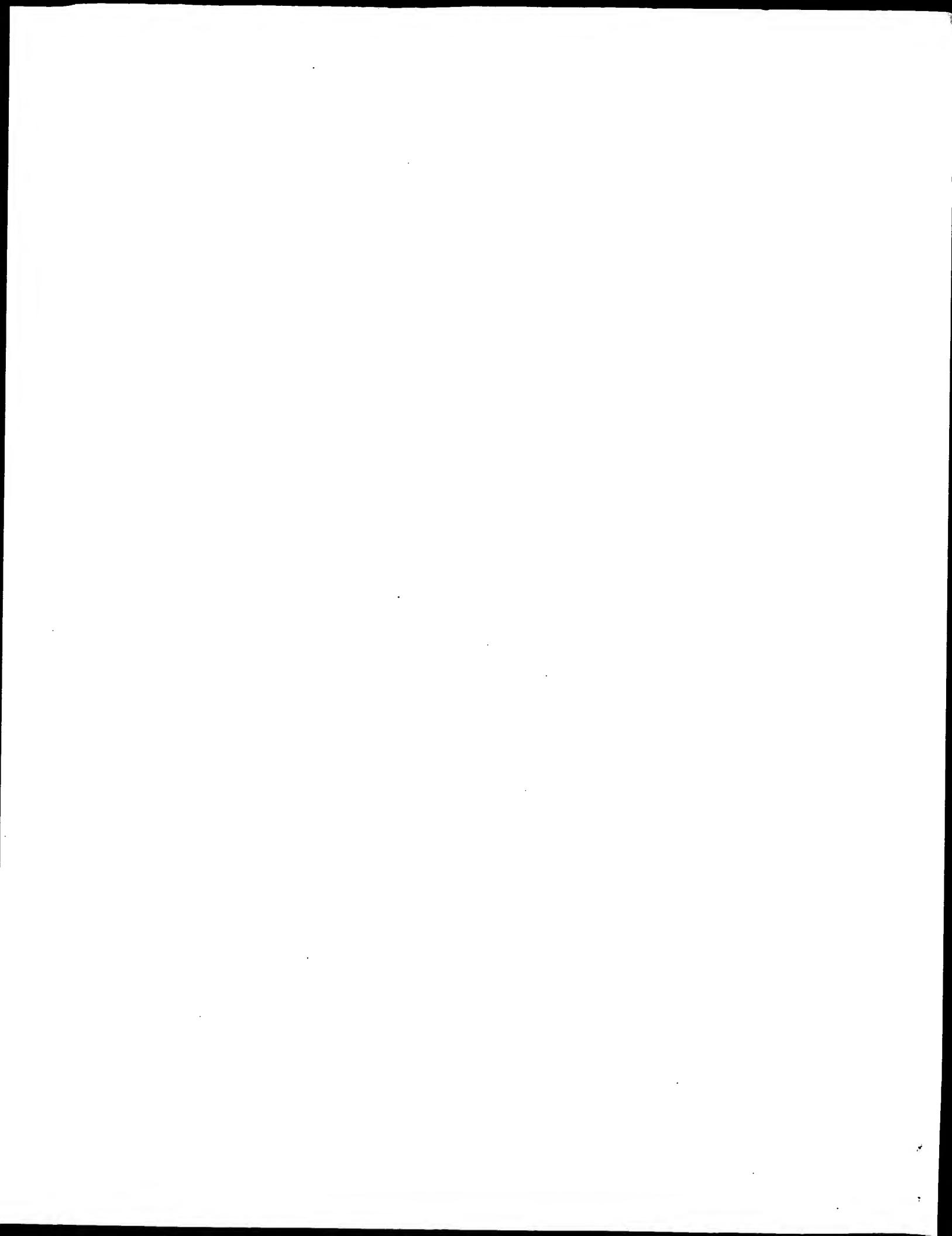
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Fri Dec 28 09:12:30 2001

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Query Match      2.1%; Score 25; DB 2; Length 157525;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
 Db 77674 TTATTTCAAAAAAAAAAAAAAAAA 77698

Search completed: December 27, 2001, 16:24:57
Job time: 5749 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:49:08 ; Search time 169.67 Seconds
(without alignments)
5927.050 Million cell updates/sec

Title: us-09-435-054-1
Perfect score: 1173
Sequence: 1 ccacgcgtccgccaccacac.....tcaaaaaaaaaaaaaaaaaa 1173

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 10

Total number of hits satisfying chosen parameters: 367515

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_1101.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173	100.0	1173	21	MAIZE LEC1 # 1 cod
2	47	4.0	1098	21	Wheat LEC1 # 3 cod
3	39	3.3	622	21	Maize LEC1 # 3 cod
4	39	3.3	763	21	Maize LEC1 # 2 cod
5	32	2.7	1121	21	Maize LEC1 # 2 c
6	26	2.2	796	21	Soybean LEC1 # 3 c
7	25	2.1	417	21	Cat flea hindgut a
8	25	2.1	417	21	Cat flea hindgut a
9	25	2.1	1234	21	Soybean neutral tr
10	25	2.1	4590	7	Sequence encoding
11	24	2.0	36	21	Reverse PCR primer

12	24	2.0	500	19	AAV73459	Flea saliva protei
13	24	2.0	500	19	AAV73460	Flea saliva protei
14	24	2.0	653	22	AAH87686	Peppermint plant o
15	24	2.0	886	21	AAH59457	Nucleotide sequenc
16	24	2.0	886	21	AAH53393	Clone se.127b04 nu
17	24	2.0	886	21	AAZ94949	Soybean glutathion
18	24	2.0	886	22	AAF31572	Soybean type I GST
19	24	2.0	1231	21	AAZ52292	Maize replication
20	24	2.0	1316	22	AAF55043	Nucleotide sequenc
21	24	2.0	1372	22	AAH24830	Nucleotide sequenc
22	24	2.0	1372	22	AAH24831	Nucleotide sequenc
23	24	2.0	1399	21	AAF16022	Human prostate can
24	24	2.0	1466	20	AAZ25133	Human hypoxia indu
25	24	2.0	1466	22	AAZ03429	Human hypoxia indu
26	24	2.0	1928	22	AAZ09829	Soybean SPFI-relat
27	24	2.0	2254	21	AAZ59457	Human secreted pro
28	24	2.0	2327	12	AAQ12152	Human transferrin
29	24	2.0	2327	21	AAZ24196	Human serum trans
30	24	2.0	2993	20	AAZ76374	Pneumocystis carin
31	23	2.0	24	20	AAZ00877	PCR primer PGR732
32	23	2.0	42	16	AAQ86155	Sindbis polyA prim
33	23	2.0	42	17	AAZ35054	Sindbis virus stra
34	23	2.0	42	17	AAZ30789	Sindbis genomic CD
35	23	2.0	42	19	AAV60127	PCR primer 4B used
36	23	2.0	42	19	AAV42366	PCR primer 4B used
37	23	2.0	42	20	AAV70686	Primer 4B used to
38	23	2.0	42	21	AAZ92767	Sindbis virus geno
39	23	2.0	42	21	AAZ92894	Sindbis virus geno
40	23	2.0	48	16	AAQ86183	Primer SINKball700
41	23	2.0	48	17	AAZ35073	Sindbis-based, tum
42	23	2.0	48	17	AAZ30807	Sindbis PCR primer
43	23	2.0	48	19	AAV42384	Reverse PCR primer
44	23	2.0	48	20	AAV70704	Reverse PCR primer
45	23	2.0	48	21	AAZ92785	Sindbis basic vect
46	23	2.0	48	21	AAZ92912	Sindbis basic vect
47	23	2.0	52	18	AAZ59252	Primer 4B used SIN
48	23	2.0	52	18	AAZ59252	Primer 4B used SIN
49	23	2.0	58	18	AAZ59240	Primer 11,703R use
50	23	2.0	58	20	AAZ59482	Reverse primer SIN
51	23	2.0	65	18	AAZ59261	Reverse primer SIN
52	23	2.0	65	20	AAZ59503	Reverse primer SIN
53	23	2.0	96	19	AAV34417	E. coli lys S gene
54	23	2.0	218	21	AAZ98737	Human colon cancer
55	23	2.0	396	22	AAZ94839	Human ovarian can
56	23	2.0	401	22	AAZ66801	Novel human polynu
57	23	2.0	437	22	AAH12484	Human cDNA clone (
58	23	2.0	612	21	AAH00804	Human irritable bo
59	23	2.0	615	17	AAZ18233	Prepro-FALt-99 CDN
60	23	2.0	683	20	AAZ61461	DNA encoding a hum
61	23	2.0	733	21	AAZ59839	Human secreted pro
62	23	2.0	753	20	AAZ87413	Hepatocellular car
63	23	2.0	758	21	AAZ01685	Human colon cancer
64	23	2.0	766	20	AAZ76970	Histamine binding
65	23	2.0	866	20	AAZ97938	Human secreted pro
66	23	2.0	893	21	AAZ65101	Membrane-bound pro
67	23	2.0	893	22	AAZ44247	Human breast tumou
68	23	2.0	906	22	AAZ55686	Human Prol185 (UNQ
69	23	2.0	1029	21	AAZ74438	Human secreted pro
70	23	2.0	1036	18	AAZ94470	Human prostate can
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74	23	2.0	1100	21	AAZ65301	DNA encoding a hum
75	23	2.0	1251	21	AAZ16249	Human secreted pro
76	23	2.0	1262	21	AAZ26404	Human prostate can
77	23	2.0	1354	21	AAZ77921	Human cancer assoc
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79	23	2.0	1453	13	AAZ22548	KDI-103 cDNA. Sin
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81	23	2.0	1506	17	AAZ95302	Murine Fas antigen
82	23	2.0	1506	16	AAZ16305	Coding sequence fo
83	23	2.0	1506	20	AAZ71961	Fas ligand (FasL)
84	23	2.0	1531	21	AAZ97040	Human secreted pro

85	23	2.0	1532	20	AA117762	Stereoselective es	c 158	22	1.9	256	21	AA16382	Human colon cancer
86	23	2.0	1550	21	AA57955	1550 bp Candida al	159	22	1.9	262	20	AAV89954	EST clone CS682
87	23	2.0	1613	20	AA230704	Rat neuronal lmed	c 160	22	1.9	321	22	AA163754	Human kidney relat
88	23	2.0	1747	21	AA98129	Human colon cancer	c 161	22	1.9	336	21	AA16503	Human colon cancer
89	23	2.0	1748	21	AA98944	Fragment of human	c 162	22	1.9	351	21	AA56526	Eucalyptus grandis
90	23	2.0	1949	13	AAQ22547	KDI-1320 cDNA. S1	c 163	22	1.9	361	22	AA565195	Novel human polynu
91	23	2.0	1963	13	AA51400	Chromosome 16q tum	c 164	22	1.9	369	21	AA311283	Plant microsatellit
92	23	2.0	1982	13	AA22546	KDI-131 cDNA. Sin	c 165	22	1.9	371	16	AAQ84711	Draculin cDNA 3' e
93	23	2.0	2027	21	AA58002	2027 bp Candida al	c 166	22	1.9	373	22	AA56534	Novel human polynu
94	23	2.0	2060	21	AA777031	Human OREF2586	c 167	22	1.9	374	22	AA565620	Human cDNA clone H
95	23	2.0	2133	18	AA96754	S. tuberosum debra	c 168	22	1.9	378	22	AA565620	Human normal ovar
96	23	2.0	2149	21	AA777736	Human cancer assoc	c 169	22	1.9	385	20	AA241260	Novel human polynu
97	23	2.0	2218	13	AAQ22551	KDI-514 cDNA. Sin	c 170	22	1.9	387	22	AA56662	Novel human polynu
98	23	2.0	2280	13	AAQ22552	KDI-554 cDNA. Sin	c 171	22	1.9	389	22	AA56594	Human prostate can
99	23	2.0	2300	18	AA762735	Herbicide-resistan	c 172	22	1.9	393	21	AA56594	Human prostate can
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102	23	2.0	2310	13	AAQ22542	KDI-350 DNA. Sind	c 175	22	1.9	407	22	AA56594	Novel human polynu
103	23	2.0	2312	13	AAQ22541	KDI-348 DNA. Sind	c 176	22	1.9	416	21	AA56594	Novel human polynu
104	23	2.0	2318	13	AAQ22540	KDI-342 DNA. Sind	c 177	22	1.9	431	21	AA56594	Novel human polynu
105	23	2.0	2319	13	AAQ22539	KDI-341 DNA. Sind	c 178	22	1.9	438	18	AAV01306	Human colon cancer
106	23	2.0	2335	13	AAQ22538	KDI-325 DNA. Sind	c 179	22	1.9	438	18	AAV01306	Human colon cancer
107	23	2.0	2353	13	AAQ22537	KDI-507 cDNA. Sin	c 180	22	1.9	439	21	AA56594	Human colon cancer
108	23	2.0	2373	17	AAQ22530	DI-25 cDNA. Sindb	c 181	22	1.9	495	18	AA56594	Human colon cancer
109	23	2.0	2435	19	AAV64580	Human PH30 beta ch	c 182	22	1.9	507	20	AA56594	Human colon cancer
110	23	2.0	2455	21	AAV64580	Tobacco chld DNA.	c 183	22	1.9	507	20	AA56594	Human colon cancer
111	23	2.0	2535	21	AAV64580	Lung cancer associ	c 184	22	1.9	549	21	AA56594	Human colon cancer
112	23	2.0	2566	22	AA774655	Mouse intracellular	c 185	22	1.9	549	21	AA56594	Human colon cancer
113	23	2.0	4203	21	AA90955	Human fatty acid d	c 186	22	1.9	566	21	AA56594	Human colon cancer
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115	23	2.0	4463	20	AA611388	DNA encoding a hum	c 188	22	1.9	571	18	AA56594	Human colon cancer
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131	23	2.0	11927	21	AA903388	Alphaviral vector	c 204	22	1.9	604	21	AA56594	Human colon cancer
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135	23	2.0	16656	16	AAQ86154	Plasmid pTRES'2J DN	c 208	22	1.9	604	21	AA56594	Human colon cancer
136	23	2.0	16656	17	AAQ86154	Eukaryotic layered	c 209	22	1.9	604	21	AA56594	Human colon cancer
137	23	2.0	16656	19	AAV60125	Alphavirus-based e	c 210	22	1.9	604	21	AA56594	Human colon cancer
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139	23	2.0	16656	19	AAV60125	Alphavirus-based e	c 212	22	1.9	604	21	AA56594	Human colon cancer
140	23	2.0	16656	21	AA292765	Representative euk	c 213	22	1.9	604	21	AA56594	Human colon cancer
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142	23	2.0	45186	22	AA560478	Wild-type human CT	c 215	22	1.9	604	21	AA56594	Human colon cancer
143	23	2.0	119950	20	AA560478	Human ves1 gene.	c 216	22	1.9	604	21	AA56594	Human colon cancer
144	23	2.0	235033	19	AAV57926	Hereditary haemoch	c 217	22	1.9	604	21	AA56594	Human colon cancer
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146	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 219	22	1.9	604	21	AA56594	Human colon cancer
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152	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 225	22	1.9	604	21	AA56594	Human colon cancer
153	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 226	22	1.9	604	21	AA56594	Human colon cancer
154	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 227	22	1.9	604	21	AA56594	Human colon cancer
155	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 228	22	1.9	604	21	AA56594	Human colon cancer
156	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 229	22	1.9	604	21	AA56594	Human colon cancer
157	23	2.0	237326	19	AAV57903	Hereditary haemoch	c 230	22	1.9	604	21	AA56594	Human colon cancer

377	22	1.9	3442	13	AAQ21623	Human Tryptophan O	450	21	1.8	389	21	AAC94591	Cat flea hindgut a
378	22	1.9	3629	19	AAA26289	Human secreted pro	451	21	1.8	389	22	AAF66032	Novel human polynu
379	22	1.9	4253	21	AAV40888	Coding sequence of	c 452	21	1.8	391	17	AAT12184	Partial pJG4-5-CDK
380	22	1.9	4253	21	AAA64156	Nucleotide sequenc	c 453	21	1.8	392	17	AAT12197	CDK4 binding prote
381	22	1.9	4253	21	AAV98453	Human CDNA clone A	c 454	21	1.8	409	21	AAA43737	Mouse secreted exp
382	22	1.9	4457	21	AAV75360	Human ORFX ORF915	c 455	21	1.8	419	22	AAF66382	Novel human polynu
383	22	1.9	5696	20	AAV37304	Human hTLP2 CDNA	c 456	21	1.8	426	22	AAH72979	Human cervical can
384	22	1.9	6107	21	AAZ98053	Human secreted pro	c 457	21	1.8	432	21	AAC59323	Human secreted pro
385	22	1.9	6107	22	AAAD11666	Human secreted pro	c 458	21	1.8	434	20	AAV30386	DNA encoding a hum
386	22	1.9	6430	20	AAV022992	Human II-lra BAC c	c 459	21	1.8	434	20	AAV30386	DNA encoding a hum
387	22	1.9	7432	19	AAV61459	Vector pPR70 conta	c 460	21	1.8	434	20	AAV30386	Maize indole-3-gl
388	22	1.9	7498	21	AAV63786	Nucleotide sequenc	c 461	21	1.8	434	20	AAV30386	Cat flea hindgut a
389	22	1.9	16225	22	AAV63786	Human breast or ov	c 462	21	1.8	434	20	AAV30386	cDNA encoding the
390	22	1.9	3152	19	AAV57791	Human colorectal c	c 463	21	1.8	434	20	AAV30386	DNA encoding a hum
391	22	1.9	35100	22	AAV20441	Human neuroblastom	c 464	21	1.8	434	20	AAV30386	probe #1804 used t
392	22	1.9	42881	22	AAV97868	Human LOMO homolog	c 465	21	1.8	434	20	AAV30386	Arabidopsis thalia
393	22	1.9	49999	20	AAZ233903	Human LOBO homolog	c 466	21	1.8	434	20	AAV30386	Human colon cancer
394	22	1.9	56516	20	AAZ00870	PGI genomic coding	c 467	21	1.8	434	20	AAV30386	Human colon cancer
395	22	1.9	56520	20	AAZ01022	Wild type PGI codi	c 468	21	1.8	434	20	AAV30386	Human secreted pro
396	22	1.9	66566	20	AAV53450	Human thiorodoxin	c 469	21	1.8	434	20	AAV30386	Cat flea hindgut a
397	22	1.9	66885	22	AAV07380	Human genomic DNA	c 470	21	1.8	434	20	AAV30386	Human secreted pro
398	22	1.9	160552	22	AAV02697	Human glycosyl sul	c 471	21	1.8	434	20	AAV30386	Human secreted pro
399	22	1.9	163319	21	AAV22306	Arabidopsis thalia	c 472	21	1.8	434	20	AAV30386	Human secreted pro
400	22	1.9	319608	22	AAV51601	Human chromosome I	c 473	21	1.8	434	20	AAV30386	Cat flea hindgut a
401	22	1.9	319608	22	AAV09301	Human schizophre	c 474	21	1.8	434	20	AAV30386	Human prostate can
402	21	1.8	27	22	AAH43080	Reverse transcript	c 475	21	1.8	434	20	AAV30386	probe #12524 used
403	21	1.8	30	17	AAT15272	Nucleotide sequenc	c 476	21	1.8	434	20	AAV30386	Parietaria allerge
404	21	1.8	34	18	AAT71288	Polyhistidine tail	c 477	21	1.8	434	20	AAV30386	DNA encoding a hum
405	21	1.8	54	19	AAV15573	Asci-HindIII gene	c 478	21	1.8	434	20	AAV30386	Fragment of GABA 9
406	21	1.8	64	15	AAQ68613	Primer for HIV RNA	c 479	21	1.8	434	20	AAV30386	Polynucleotide cto
407	21	1.8	64	17	AAT09933	trNAPOLYU primer #	c 480	21	1.8	434	20	AAV30386	Fusarium venenatum
408	21	1.8	76	18	AAT90806	Mouse persepchin ge	c 481	21	1.8	434	20	AAV30386	Human secreted pro
409	21	1.8	76	20	AAV60475	W09914235 Seg ID N	c 482	21	1.8	434	20	AAV30386	Pathogen response
410	21	1.8	155	22	AAI27706	Probe #17639 for g	c 483	21	1.8	434	20	AAV30386	Human secreted pro
411	21	1.8	184	22	AAH22416	Probe #23357 used	c 484	21	1.8	434	20	AAV30386	Human secreted pro
412	21	1.8	184	22	AAH22416	Mouse hexokinase I	c 485	21	1.8	434	20	AAV30386	Human secreted pro
413	21	1.8	236	22	AAH72201	Human cervical can	c 486	21	1.8	434	20	AAV30386	Fusarium venenatum
414	21	1.8	244	21	AAH55136	Human secreted pro	c 487	21	1.8	434	20	AAV30386	Human secreted pro
415	21	1.8	244	21	AAH55136	Human secreted pro	c 488	21	1.8	434	20	AAV30386	Human colon cancer
416	21	1.8	248	21	AAV95297	Cat flea head and	c 489	21	1.8	434	20	AAV30386	Human colon cancer
417	21	1.8	270	21	AAH31441	Plant microsatelli	c 490	21	1.8	434	20	AAV30386	Soybean cyclin-dep
418	21	1.8	270	22	AAH71139	Human cervical can	c 491	21	1.8	434	20	AAV30386	Partial human DNAX
419	21	1.8	276	22	AAH69336	Human secreted pro	c 492	21	1.8	434	20	AAV30386	Human breast tumou
420	21	1.8	282	22	AAV07747	Cervical cancer pr	c 493	21	1.8	434	20	AAV30386	Human cancer assoc
421	21	1.8	296	21	AAV00871	Human colon cancer	c 494	21	1.8	434	20	AAV30386	Human cancer 7001028
422	21	1.8	304	21	AAH00871	Human secreted pro	c 495	21	1.8	434	20	AAV30386	Corn clone 7001028
423	21	1.8	307	22	AAH72404	Human secreted pro	c 496	21	1.8	434	20	AAV30386	Human secreted pro
424	21	1.8	311	22	AAH70853	Human cervical can	c 497	21	1.8	434	20	AAV30386	Human secreted pro
425	21	1.8	325	21	AAV99965	Human secreted pro	c 498	21	1.8	434	20	AAV30386	Human secreted pro
426	21	1.8	331	22	AAH69518	Human secreted pro	c 499	21	1.8	434	20	AAV30386	Human secreted pro
427	21	1.8	340	22	AAH87797	Peppermint plant o	c 500	21	1.8	434	20	AAV30386	Human secreted pro
428	21	1.8	345	22	AAH33454	Human colon cancer	c 501	21	1.8	434	20	AAV30386	Human secreted pro
429	21	1.8	348	21	AAV94880	Human colon cancer	c 502	21	1.8	434	20	AAV30386	Human secreted pro
430	21	1.8	368	22	AAV64984	Cat flea hindgut a	c 503	21	1.8	434	20	AAV30386	Human secreted pro
431	21	1.8	372	22	AAH88004	Novel human polynu	c 504	21	1.8	434	20	AAV30386	Human secreted pro
432	21	1.8	376	21	AAV15926	Peppermint plant o	c 505	21	1.8	434	20	AAV30386	Human secreted pro
433	21	1.8	378	21	AAV74350	Human secreted pro	c 506	21	1.8	434	20	AAV30386	Human secreted pro
434	21	1.8	378	22	AAV91758	Human 10 kb Clara	c 507	21	1.8	434	20	AAV30386	Strawberry alcohol
435	21	1.8	382	22	AAV64646	Novel human polynu	c 508	21	1.8	434	20	AAV30386	Strawberry alcohol
436	21	1.8	383	19	AAV61297	cDNA sequence of p	c 509	21	1.8	434	20	AAV30386	Human colon cancer
437	21	1.8	383	19	AAV58559	prostate tumour sp	c 510	21	1.8	434	20	AAV30386	Human secreted pro
438	21	1.8	383	21	AAV06332	Human immunogenic	c 511	21	1.8	434	20	AAV30386	Human secreted pro
439	21	1.8	383	22	AAV10081	Human prostate tum	c 512	21	1.8	434	20	AAV30386	Human secreted pro
440	21	1.8	383	22	AAH93438	Human prostate-spe	c 513	21	1.8	434	20	AAV30386	Human secreted pro
441	21	1.8	383	22	AAH84752	Human prostate-spe	c 514	21	1.8	434	20	AAV30386	Human secreted pro
442	21	1.8	383	22	AAH02503	Prostate tumour an	c 515	21	1.8	434	20	AAV30386	Human secreted pro
443	21	1.8	384	19	AAV61328	Extended cDNA sequ	c 516	21	1.8	434	20	AAV30386	Human secreted pro
444	21	1.8	384	19	AAV58653	Prostate tumour sp	c 517	21	1.8	434	20	AAV30386	Human secreted pro
445	21	1.8	384	21	AAV06416	Human immunogenic	c 518	21	1.8	434	20	AAV30386	Human secreted pro
446	21	1.8	384	22	AAV10175	Human prostate tum	c 519	21	1.8	434	20	AAV30386	Human secreted pro
447	21	1.8	384	22	AAH93532	Human prostate-spe	c 520	21	1.8	434	20	AAV30386	Human secreted pro
448	21	1.8	384	22	AAH84846	Human prostate-spe	c 521	21	1.8	434	20	AAV30386	Sequence encoding
449	21	1.8	384	22	AAH02597	Prostate tumour an	c 522	21	1.8	434	20	AAV30386	Human secreted pro

523	21	1.8	747	21	AA12354	Aspergillus oryzae	596	21	1.8	1063	19	AAV11154	Human EST cDNA. H
524	21	1.8	750	21	AA01845	Human colon cancer	597	21	1.8	1063	19	AAV12466	Human oestrogen su
525	21	1.8	769	21	AA09474	Human secreted pro	598	21	1.8	1072	21	AA04137	Nucleotide sequenc
526	21	1.8	770	21	AA05523	Human secreted pro	599	21	1.8	1074	19	AAV23874	Plant OMT enzyme D
527	21	1.8	771	21	AAZ16417	Human gene express	600	21	1.8	1074	21	AA06877	Pine O-methyl tran
528	21	1.8	772	21	AAZ44851	Human breast cance	601	21	1.8	1074	21	AA067961	Pinus radiata OMT
529	21	1.8	779	21	AA161193	Human prostate can	602	21	1.8	1075	19	AAV23875	Plant OMT enzyme D
530	21	1.8	780	18	AA159912	Human transcrip tio	603	21	1.8	1075	20	AA06878	Pine O-methyl tran
531	21	1.8	781	21	AAZ15665	Human gene express	604	21	1.8	1075	21	AA067962	Pinus radiata OMT
532	21	1.8	792	21	AA080905	Human cDNA clone H	605	21	1.8	1082	21	AA15337	Nucleic acid encod
533	21	1.8	798	22	AAH70954	Human cervical can	606	21	1.8	1082	22	AA02648	Human secreted pro
534	21	1.8	801	21	AA018855	Human colon cancer	607	21	1.8	1092	22	AAH31375	Human secreted pro
535	21	1.8	803	22	AA097933	Human secreted pro	608	21	1.8	1094	21	AA059452	Protein PRO303 cDN
536	21	1.8	804	20	AA061470	DNA encoding a hum	609	21	1.8	1100	22	AA052259	Human PRO303 cDN
537	21	1.8	808	20	AA043514	Human secreted pro	610	21	1.8	1100	22	AA072417	Human secreted pro
538	21	1.8	810	21	AA079975	Human secreted pro	611	21	1.8	1104	21	AA069085	Human secreted pro
539	21	1.8	817	20	AAZ24433	Human bladder tumo	612	21	1.8	1110	22	AA089726	Maize ZmGnsN1-4 g1
540	21	1.8	820	19	AA035168	Thuga plicata diri	613	21	1.8	1112	21	AA013890	Aspergillus oryzae
541	21	1.8	820	22	AA012503	Thuja plicata diri	614	21	1.8	1117	19	AAV59118	Nucleotide sequenc
542	21	1.8	822	20	AA037413	Human secreted pro	615	21	1.8	1135	21	AA093433	Human secreted pro
543	21	1.8	826	20	AA099893	Fragment of aspart	616	21	1.8	1139	9	AA080299	Interleukin 6. A
544	21	1.8	835	20	AAZ15794	Human gene express	617	21	1.8	1139	10	AA090255	Interleukin-6. Ho
545	21	1.8	845	21	AAZ49560	Maize MLO1 protein	618	21	1.8	1148	20	AA039615	Breast cancer asso
546	21	1.8	847	21	AA077942	Human cancer assoc	619	21	1.8	1160	20	AA061434	DNA encoding a hum
547	21	1.8	850	22	AA055765	Human SCN1A genomi	620	21	1.8	1163	20	AA034369	Human fibroblast g
548	21	1.8	854	21	AA093453	Human secreted pro	621	21	1.8	1181	21	AA095415	Cat flea HNC anoxi
549	21	1.8	858	19	AAV35161	Human secreted pro	622	21	1.8	1181	21	AA095416	Cat flea HNC Aup h
550	21	1.8	858	22	AA012496	Forsythia dirigent	623	21	1.8	1182	21	AA078424	Human secreted pro
551	21	1.8	865	20	AA025145	Forsythia intermed	624	21	1.8	1196	21	AA026350	Human secreted pro
552	21	1.8	866	22	AA013355	Wheat Type I gluta	625	21	1.8	1200	21	AA033359	Human secreted pro
553	21	1.8	866	22	AA013384	Human secreted pro	626	21	1.8	1200	22	AA0158676	Human polynucleoti
554	21	1.8	872	22	AA007635	Human secreted pro	627	21	1.8	1204	22	AA0163823	Human polynucleoti
555	21	1.8	883	20	AA024819	Human secreted pro	628	21	1.8	1205	20	AA024236	Human normal bladd
556	21	1.8	886	21	AA045888	cDNA encoding a hu	629	21	1.8	1214	22	AA011360	Rice DNA encoding
557	21	1.8	889	20	AA037509	Human secreted pro	630	21	1.8	1217	20	AA024836	Human secreted pro
558	21	1.8	893	16	AA092529	P. communis (pear)	631	21	1.8	1227	21	AA076393	Human ORFX ORF1948
559	21	1.8	900	20	AA027548	Maize glutathione-	632	21	1.8	1232	22	AA079859	Vitis cis-prenyltr
560	21	1.8	901	21	AA0294788	Maize class I glut	633	21	1.8	1233	21	AA045159	Rat 20alpha-hydrox
561	21	1.8	901	21	AA076253	Maize glutathione-	634	21	1.8	1236	19	AA048114	Nucleotide sequenc
562	21	1.8	902	21	AA080562	Human secreted pro	635	21	1.8	1250	21	AA059054	Human secreted pro
563	21	1.8	905	21	AA027457	Veronia mespilifol	636	21	1.8	1253	22	AA034294	Human colon cancer
564	21	1.8	911	21	AA076267	Maize glutathione-	637	21	1.8	1260	22	AA054599	Human secreted pro
565	21	1.8	920	22	AA063855	Human polynucleoti	638	21	1.8	1263	21	AA090460	Human uncoupling p
566	21	1.8	921	20	AA027330	Human secreted pro	639	21	1.8	1267	8	AA070806	Sequence of cDNA c
567	21	1.8	928	20	AA000804	Human secreted pro	640	21	1.8	1267	14	AA037483	Elmeria tenella TA
568	21	1.8	930	20	AA066433	Human secreted pro	641	21	1.8	1272	21	AA036232	cDNA encoding a bo
569	21	1.8	935	20	AA010780	Trehalose-6-phosph	642	21	1.8	1273	20	AA006777	Human sperm-specif
570	21	1.8	935	21	AA069418	Human secreted pro	643	21	1.8	1276	21	AA074265	Human secreted pro
571	21	1.8	942	10	AA090111	Fish growth hormon	644	21	1.8	1284	12	AA015361	NF-YB. Homo sapie
572	21	1.8	942	18	AA091594	Calliphora vomitor	645	21	1.8	1286	21	AA056341	Pinus radiata tran
573	21	1.8	944	12	AA010912	Fish growth hormon	646	21	1.8	1290	21	AA095494	Human secreted pro
574	21	1.8	951	20	AA084598	Human secreted pro	647	21	1.8	1295	21	AA040192	H. vulgare nicotia
575	21	1.8	958	21	AA039360	Arabidopsis thalia	648	21	1.8	1311	21	AA0297134	Human secreted pro
576	21	1.8	967	21	AA076276	Maize glutathione-	649	21	1.8	1314	21	AA040194	H. vulgare nicotia
577	21	1.8	969	22	AA072746	Human prostate can	650	21	1.8	1319	20	AA086119	cDNA encoding a tr
578	21	1.8	974	20	AA086122	DNA encoding a Tr	651	21	1.8	1325	20	AA080740	Human secreted pro
579	21	1.8	983	20	AA084445	Human secreted pro	652	21	1.8	1327	22	AA033751	Human colon cancer
580	21	1.8	999	20	AA080678	Human DNAX toll-li	653	21	1.8	1327	22	AA007864	Human secreted pro
581	21	1.8	1000	22	AA032566	Human secreted pro	654	21	1.8	1328	21	AA087747	Human secreted pro
582	21	1.8	1006	21	AA0712641	Aspergillus oryzae	655	21	1.8	1328	22	AA064029	cDNA encoding huma
583	21	1.8	1006	21	AA077762	Human cancer assoc	656	21	1.8	1331	22	AA091776	Sunflower seedling
584	21	1.8	1008	22	AA011576	Human cDNA encodin	657	21	1.8	1338	15	AA065607	Rabbit zona pelluc
585	21	1.8	1008	22	AA0502400	Human secreted pro	658	21	1.8	1338	20	AA022712	Rabbit zona pelluc
586	21	1.8	1009	22	AA089952	Human camello 1 (H	659	21	1.8	1338	20	AA064789	Rabbit zona pelluc
587	21	1.8	1012	20	AA021219	zea mays eIF-4E pr	660	21	1.8	1338	21	AA0295649	Rabbit oocyte zona
588	21	1.8	1015	21	AA059665	Human secreted pro	661	21	1.8	1338	21	AA046257	Rabbit zona pelluc
589	21	1.8	1018	20	AA061378	DNA encoding a hum	662	21	1.8	1338	21	AA033246	Rabbit zona pelluc
590	21	1.8	1037	20	AA030150	Human secreted pro	663	21	1.8	1339	21	AA037801	Rabbit zona pelluc
591	21	1.8	1042	21	AA064191	Nucleotide sequenc	664	21	1.8	1339	21	AA099968	Human secreted pro
592	21	1.8	1046	12	AA010337	Plasmid pMG3C9 use	665	21	1.8	1358	22	AA033867	Human colon cancer
593	21	1.8	1046	12	AA010337	Mouse Glutamine re	666	21	1.8	1365	16	AA087044	Pig interleukin-10
594	21	1.8	1061	21	AA047442	Human TANGO 221 co	667	21	1.8	1365	16	AA085772	Porcine interleuki
595	21	1.8	1062	21	AA089455	Corn branched chai	668	21	1.8	1366	21	AA016216	Human prostate can

669	21	1.8	1374	21	AAC90077	Human pancreatic c	742	21	1.8	1707	22	AAD05834	Arabidopsis thalia
670	21	1.8	1379	22	AAH50828	Arabidopsis thalia	743	21	1.8	1707	22	AAF80403	Nucleotide sequenc
671	21	1.8	1381	22	AAD50964	sterol C5 desatura	744	21	1.8	1710	20	AAF99953	Nucleotide sequenc
672	21	1.8	1389	20	AAX27067	Original S. tubero	745	21	1.8	1712	21	AAC76982	Human ORFX ORF2537
673	21	1.8	1391	20	AAX27358	Human secreted pro	746	21	1.8	1714	22	AAD05590	Human secreted pro
674	21	1.8	1392	22	AAD05340	Human secreted pro	747	21	1.8	1720	21	AAA33471	Human secreted pro
675	21	1.8	1393	21	AA59441	Nucleotide sequenc	748	21	1.8	1724	20	AAZ20442	Human AD2 DNA. H
676	21	1.8	1393	22	AA63797	Human secreted pro	749	21	1.8	1733	16	AAQ84046	Human secreted pro
677	21	1.8	1410	22	AA98169	Human colon cancer	750	21	1.8	1733	17	AAAT18102	Japonicum allergen
678	21	1.8	1410	22	AAH34321	Human colon cancer	751	21	1.8	1733	21	AAA54528	phytyl/prenyltrans
679	21	1.8	1411	21	AAA26308	Human secreted pro	752	21	1.8	1743	21	AAAF3089	Human PRO1337 (UNO
680	21	1.8	1420	21	AAAT78510	Plant SDF polynucl	753	21	1.8	1743	22	AAF54367	Primer #140 used i
681	21	1.8	1428	20	AAX24403	Maize secreted pro	754	21	1.8	1747	21	AAA93128	Human secreted pro
682	21	1.8	1433	15	AAQ65397	Maize myo-inositol	755	21	1.8	1752	21	AAZ38575	D. farinae mite al
683	21	1.8	1433	16	AAQ92306	Elm ClO:O-acyl car	756	21	1.8	1752	21	AAZ38576	D. farinae mite al
684	21	1.8	1433	17	AAQ92306	Elm class II thioe	757	21	1.8	1753	22	AAAS00149	Human cDNA clone H
685	21	1.8	1433	19	AAQ36108	Elm acyl-ACP thioe	758	21	1.8	1756	21	AAAF16318	Human prostate can
686	21	1.8	1433	19	AAV15230	ClO:O-ACP thioeste	759	21	1.8	1758	20	AAZ07159	Human lung tumour
687	21	1.8	1437	20	AAZ22859	Maize indole-3-gly	760	21	1.8	1758	21	AAZ07159	Human lung tumour
688	21	1.8	1442	19	AAZ25906	Rat aquaporin-5 en	761	21	1.8	1781	21	AAA53979	p33 tumour suppress
689	21	1.8	1442	20	AAQ06779	Human sperm-specif	762	21	1.8	1781	21	AAA53979	p33 tumour suppress
690	21	1.8	1442	20	AAQ04106	Rat aquaporin-5 en	763	21	1.8	1808	21	AAAF16342	Human prostate can
691	21	1.8	1443	19	AAV69815	Human secreted pro	764	21	1.8	1808	22	AAF91897	Human secreted pro
692	21	1.8	1448	21	AAV59796	Human secreted pro	765	21	1.8	1810	21	AAAC59143	Human secreted pro
693	21	1.8	1457	21	AAAC53822	Arabidopsis thalia	766	21	1.8	1816	20	AAZ52977	Human prostate tum
694	21	1.8	1459	22	AAAF72816	Secreted protein g	767	21	1.8	1821	22	AAAF97932	Human secreted pro
695	21	1.8	1465	21	AAA78406	Human secreted pro	768	21	1.8	1844	22	AAAF64372	GABA-gated chlorid
696	21	1.8	1467	21	AAAC59814	Human secreted pro	769	21	1.8	1844	21	AAAF16260	Human prostate can
697	21	1.8	1476	21	AAAC79683	Human secreted pro	770	21	1.8	1849	21	AAAF4936	cDNA encoding a hu
698	21	1.8	1477	21	AAAC5865	Human secreted pro	771	21	1.8	1849	21	AAZ57314	Human endokine alp
699	21	1.8	1502	20	AAH59131	Human secreted pro	772	21	1.8	1862	21	AAAF16048	Human prostate can
700	21	1.8	1502	21	AAAD01239	Human interferon-e	773	21	1.8	1862	22	AAAF32779	Human secreted pro
701	21	1.8	1503	20	AAZ26295	Aspen bispecific O	774	21	1.8	1873	22	AAAF76766	Human ORFX ORF2321
702	21	1.8	1504	21	AAAC59799	Human secreted pro	775	21	1.8	1884	22	AAAH41367	Rat betaine homocy
703	21	1.8	1512	21	AACT77808	Human cancer assoc	776	21	1.8	1892	20	AAZ24890	Human secreted pro
704	21	1.8	1515	17	AAAT07072	Adhesive protein g	777	21	1.8	1892	21	AAAF21834	Human breast and o
705	21	1.8	1515	21	AAAT18219	Lung cancer associ	778	21	1.8	1896	21	AAAF21834	Human breast and o
706	21	1.8	1520	21	AAAC64786	Human acyl transfe	779	21	1.8	1899	20	AAAX06785	Human MTC49 cDNA
707	21	1.8	1532	21	AAZ43804	Human adult brain	780	21	1.8	1899	21	AAAC39113	Arabidopsis thalia
708	21	1.8	1532	22	AAH34454	Human colon cancer	781	21	1.8	1900	22	AAAF63417	Human CB39-L2 spli
709	21	1.8	1555	21	AACT77385	Human ORFX ORF2940	782	21	1.8	1910	22	AAAF63417	Nucleotide sequenc
710	21	1.8	1556	22	AAD05528	Human secreted pro	783	21	1.8	1916	22	AAD10862	Arabidopsis thalia
711	21	1.8	1558	16	AAQ85986	Raphanus sativus p	784	21	1.8	1918	21	AAAC93456	Human secreted pro
712	21	1.8	1559	20	AAZ25211	Maize cinnamoyl-Co	785	21	1.8	1923	22	AAAC93456	Human secreted pro
713	21	1.8	1574	21	AACT78187	Human cancer assoc	786	21	1.8	1928	18	AAAT95762	Arabidopsis SCLa7
714	21	1.8	1574	22	AAAF32743	Human secreted pro	787	21	1.8	1928	21	AAAC65290	Arabidopsis SCLa7
715	21	1.8	1583	21	AAZ65262	Human secreted pro	788	21	1.8	1930	22	AAAF1891	Human secreted pro
716	21	1.8	1588	21	AAAD00809	Human irritabile bo	789	21	1.8	1931	22	AAH33913	Human colon cancer
717	21	1.8	1598	22	AAD05306	Human secreted pro	790	21	1.8	1931	22	AAAF63608	PERP (p53 apoptosi
718	21	1.8	1601	21	AAAF15881	Human prostate can	791	21	1.8	1935	19	AAAS9638	Human secreted pro
719	21	1.8	1608	19	AAV04610	Human cathepsin X	792	21	1.8	1948	20	AAZ00470	Human secreted pro
720	21	1.8	1614	22	AAAF85155	Nucleotide sequenc	793	21	1.8	1952	21	AAAC59577	Human secreted pro
721	21	1.8	1615	20	AAZ41318	Human normal ovary	794	21	1.8	1964	21	AAAC98066	Human colon cancer
722	21	1.8	1619	16	AAAT04002	Human osteoclast-d	795	21	1.8	1969	21	AAZ56461	Human myosin heavy
723	21	1.8	1619	20	AAZ20647	CBMACD04 coding se	796	21	1.8	1969	22	AAAS00510	Human secreted pro
724	21	1.8	1636	15	AAQ58006	Sequence of plasm	797	21	1.8	1977	21	AAZ27383	Human secreted pro
725	21	1.8	1638	17	AAAT06480	Cystathionine gamm	798	21	1.8	1977	21	AAAC98890	Human pancreatic c
726	21	1.8	1680	20	AAZ41986	Human endometrium	799	21	1.8	1985	21	AAAC59406	Human secreted pro
727	21	1.8	1645	21	AAAB88851	Maize geranylgeran	800	21	1.8	2004	21	AAAF16298	Human prostate can
728	21	1.8	1655	21	AAZ61589	DNA encoding a hum	801	21	1.8	2006	21	AAAF15839	Human prostate can
729	21	1.8	1655	21	AAZ61589	DNA encoding a hum	802	21	1.8	2006	21	AAA52777	Wheat putative cat
730	21	1.8	1660	17	AAT39663	Sia alpha 2,3Gal B	803	21	1.8	2006	21	AAZ6363	Human secreted pro
731	21	1.8	1661	21	AAAC59172	Human secreted pro	804	21	1.8	2030	21	AAAC39965	Murine TANGO 185 c
732	21	1.8	1662	21	AAC76592	Human secreted pro	805	21	1.8	2032	21	AAAC98080	Human colon cancer
733	21	1.8	1669	22	AAH84226	Human cell death p	806	21	1.8	2043	21	AAAF22359	Human secreted pro
734	21	1.8	1676	20	AAAX97974	Human secreted pro	807	21	1.8	2043	22	AAH33065	Human colon cancer
735	21	1.8	1680	22	AAAS11575	Human cDNA encodin	808	21	1.8	2069	20	AAZ32727	Neospora caninum M
736	21	1.8	1691	21	AAAC98774	Human pancreatic c	809	21	1.8	2069	20	AAAI9490	Human secreted pro
737	21	1.8	1691	21	AACT79830	Human secreted pro	810	21	1.8	2070	19	AAV40692	Kir3.1/KGA coding
738	21	1.8	1697	22	AAAS01144	Human steroid horm	811	21	1.8	2076	16	AAQ75355	Potassium KGA chan
739	21	1.8	1701	19	AAV15617	Tobacco invertase	812	21	1.8	2084	21	AACT76364	Human ORFX ORF1919
740	21	1.8	1701	19	AAV10235	Tobacco invertase	813	21	1.8	2094	21	AAAT1623	Human aspartate pr
741	21	1.8	1702	22	AAI59301	Human polynucleoti	814	21	1.8	2109	21	AAZ52769	Corn putative cata
												AAZ59417	Wheat copalyl diph

815	21	1.8	2119	14	AAQ43853	Sequence of part o	888	21	1.8	2970	22	AAF33249	Human secreted pro
c 816	21	1.8	2135	22	AAQ39216	Arabidopsis thalia	c 889	21	1.8	3034	21	AAQ57984	3034 bp Candida al
817	21	1.8	2142	22	AAQ72840	Secreted protein g	890	21	1.8	3090	20	AAQ89079	Nucleotide sequenc
818	21	1.8	2143	22	AAQ07938	Human secreted pro	891	21	1.8	3090	21	AAQ27033	Human c-cbl CDNA w
819	21	1.8	2154	21	AAQ55156	Arabidopsis thalia	892	21	1.8	3101	19	AAQ32918	Solanum tuberosum
820	21	1.8	2156	20	AAQ10807	Polynucleotide seq	893	21	1.8	3417	21	AAQ70163	Plasmodium falcipa
c 821	21	1.8	2161	19	AAQ07919	Helicobacter pylori	894	21	1.8	3427	21	AAQ67946	Human ORF ORF2501
822	21	1.8	2173	21	AAQ00810	Human irritable bo	c 895	21	1.8	3471	14	AAQ46673	p mySB CDNA clone.
823	21	1.8	2178	22	AAQ98380	Human CDNA clone B	896	21	1.8	3511	21	AAQ96933	Human secreted pro
824	21	1.8	2190	20	AAQ24407	Human bladder tumo	897	21	1.8	3522	22	AAQ07590	Human secreted pro
825	21	1.8	2207	20	AAQ03845	Partial human 7-tr	898	21	1.8	3568	21	AAQ99491	DNA encoding a mai
826	21	1.8	2219	18	AAQ78852	Human cyclin G1 cD	899	21	1.8	3686	22	AAQ85358	Murine SOCS-3 prom
827	21	1.8	2236	21	AAQ00311	Human Ras signalli	900	21	1.8	3693	21	AAQ33335	Human secreted pro
828	21	1.8	2273	22	AAQ162754	Human CDNA SEQ ID	901	21	1.8	3696	22	AAQ72827	Secreted protein g
829	21	1.8	2273	22	AAQ33306	Human colon cancer	902	21	1.8	3707	22	AAQ08367	Human secreted pro
830	21	1.8	2287	21	AAQ69105	Human secreted pro	903	21	1.8	3734	22	AAQ21317	Human CDNA sequenc
831	21	1.8	2287	22	AAQ07819	Human secreted pro	904	21	1.8	3784	11	AAQ05326	Sequence of new pl
832	21	1.8	2288	22	AAQ97897	Human secreted pro	905	21	1.8	3850	9	AAQ81634	Yellowtail tuna DN
833	21	1.8	2294	22	AAQ63419	Human CD39-L2 spli	906	21	1.8	3851	18	AAQ79857	Intron 3 of human
834	21	1.8	2324	21	AAQ48578	CDNA encoding whea	907	21	1.8	3851	18	AAQ79857	Murine SOCS-3 prom
835	21	1.8	2326	20	AAQ85833	DNA encoding human	908	21	1.8	3865	18	AAQ96833	Human PRO1012 nucl
836	21	1.8	2326	22	AAQ31279	Human mammatatin	909	21	1.8	3940	22	AAQ85356	Human PRO1012 (UNQ
837	21	1.8	2329	20	AAQ31844	Human 7-transmembr	910	21	1.8	4040	20	AAQ34275	Human CDNA sequenc
838	21	1.8	2330	22	AAQ09285	Human TANGO 457 cD	911	21	1.8	4040	21	AAQ78573	Human lung tumour
839	21	1.8	2353	19	AAQ45981	A. thaliana sterol	912	21	1.8	4040	22	AAQ21456	Human ORF ORF3038
840	21	1.8	2371	21	AAQ18222	Lung cancer associ	913	21	1.8	4235	22	AAQ68399	Human ORF ORF2089
841	21	1.8	2371	22	AAQ63416	Human CD39-L2 spli	914	21	1.8	4668	21	AAQ77483	Mouse P4P6B1 OMA (
842	21	1.8	2376	20	AAQ72590	Mouse neurotropsin	c 915	21	1.8	4763	21	AAQ76534	Human CDNA sequenc
843	21	1.8	2383	21	AAQ18298	Lung cancer associ	916	21	1.8	4938	22	AAQ02457	Human WART2 CDNA.
844	21	1.8	2384	20	AAQ36895	Human ABC-Transpor	917	21	1.8	5276	20	AAQ87397	Promoter of gene r
845	21	1.8	2401	22	AAQ56506	Arabidopsis CDC27A	c 918	21	1.8	5538	22	AAQ18660	Human IL-1ra BAC c
846	21	1.8	2434	22	AAQ56505	Arabidopsis CDC27A	919	21	1.8	6298	22	AAQ75767	Zucchini ACC synth
847	21	1.8	2466	22	AAQ32255	Human secreted pro	c 920	21	1.8	6727	20	AAQ02993	Zucchini CP-ACC 1B
848	21	1.8	2471	21	AAQ29050	Human prostate ser	c 921	21	1.8	7587	12	AAQ15133	Zucchini ACC synth
849	21	1.8	2496	19	AAQ63189	CDNA from clone cr	c 922	21	1.8	7587	19	AAQ15703	Human LMP-1 (HLMF-
850	21	1.8	2497	22	AAQ63421	Human CD39-L2 spli	c 923	21	1.8	7587	22	AAQ04543	Human LMP-1 (HLMF-
851	21	1.8	2509	22	AAQ51464	Human secreted pro	c 924	21	1.8	7587	22	AAQ23620	Human glycosyl sul
852	21	1.8	2567	19	AAQ44889	Coding sequence fo	925	21	1.8	8743	20	AAQ99284	Human colorectal c
853	21	1.8	2567	21	AAQ98602	Human p56-2 nucleo	926	21	1.8	9741	22	AAQ06120	Human low adenosin
854	21	1.8	2570	22	AAQ87061	Nucleotide sequenc	927	21	1.8	9854	22	AAQ35185	Human ABC1 DNA seq
855	21	1.8	2575	20	AAQ10654	CDNA encoding a hu	928	21	1.8	11492	20	AAQ74107	Human adenosine re
856	21	1.8	2584	20	AAQ10676	CDNA encoding a hu	c 929	21	1.8	14740	21	AAQ87743	Human low adenosin
857	21	1.8	2599	21	AAQ76501	Human ORF ORF2056	930	21	1.8	27150	22	AAQ02701	Human adenosine re
858	21	1.8	2610	21	AAQ33371	Human secreted pro	c 931	21	1.8	32204	22	AAQ51594	Human genomic sequ
c 859	21	1.8	2634	16	AAQ87841	Human neuronal cal	c 932	21	1.8	32351	21	AAQ57790	Nucleotide sequenc
c 860	21	1.8	2634	21	AAQ71722	Human calcium chan	c 933	21	1.8	32351	21	AAQ21307	Human chromosome 6
861	21	1.8	2654	20	AAQ88500	Human huplin/pi 13	c 934	21	1.8	40298	21	AAQ35185	Human adenosine re
862	21	1.8	2671	17	AAQ33648	Ras p21 interactin	c 935	21	1.8	40298	21	AAQ21311	Human ELAM-1 polyn
863	21	1.8	2671	20	AAQ09608	Human RGL CDNA. H	c 936	21	1.8	49312	21	AAQ35189	Human low adenosin
864	21	1.8	2672	21	AAQ16680	Human secreted pro	c 937	21	1.8	50000	21	AAQ64139	Human low adenosin
865	21	1.8	2693	22	AAQ63418	Human CD39-L2 spli	938	21	1.8	68940	20	AAQ57351	Human adenosine re
866	21	1.8	2700	22	AAQ33268	Human colon cancer	939	21	1.8	138169	21	AAQ34791	Human ELAM-1 polyn
c 867	21	1.8	2712	16	AAQ87836	Human neuronal cal	940	21	1.8	141589	21	AAQ20913	Human low adenosin
c 868	21	1.8	2712	21	AAQ71733	Human calcium chan	c 941	21	1.8	141589	21	AAQ21127	Human low adenosin
c 869	21	1.8	2754	21	AAQ49068	Arabidopsis thalia	942	21	1.8	141589	21	AAQ21152	Human low adenosin
870	21	1.8	2762	21	AAQ96066	Human ecto-phospha	943	21	1.8	141589	21	AAQ35005	Human adenosine re
871	21	1.8	2762	22	AAQ63386	Human CD39-L2 codi	944	21	1.8	141589	21	AAQ35030	Human adenosine re
872	21	1.8	2762	22	AAQ63422	Human CD39-L2 spli	945	21	1.8	146981	21	AAQ21442	Human ELAM-1 polyn
873	21	1.8	2789	21	AAQ93521	Human secreted pro	946	21	1.8	209273	21	AAQ21437	Human factor-relat
874	21	1.8	2805	22	AAQ63420	Human CD39-L2 spli	c 947	21	1.8	1082138	21	AAQ22305	Arabidopsis thalia
875	21	1.8	2812	16	AAQ02327	Human fibroblast a	c 948	20	1.7	20	16	AAQ75564	Reverse transcript
876	21	1.8	2815	18	AAQ90148	Human fibroblast a	c 949	20	1.7	20	21	AAQ27451	LEC1 primer # 1.
877	21	1.8	2818	20	AAQ89286	Human fibroblast a	c 950	20	1.7	20	21	AAQ27452	LEC1 primer # 2.
878	21	1.8	2818	20	AAQ87710	Human Burkitt's ly	c 951	20	1.7	20	21	AAQ27453	LEC1 primer # 3.
879	21	1.8	2831	21	AAQ98739	Human serum prote	c 952	20	1.7	20	21	AAQ27454	LEC1 primer # 4.
880	21	1.8	2832	20	AAQ88499	Human hirpin/pi 13	c 953	20	1.7	21	16	AAQ75629	Reverse transcript
881	21	1.8	2848	21	AAQ16656	Human secreted pro	c 954	20	1.7	21	16	AAQ75630	Reverse transcript
882	21	1.8	2863	22	AAQ85357	Murine SOCS-3 prom	c 955	20	1.7	21	16	AAQ75627	Reverse transcript
883	21	1.8	2868	19	AAQ55968	Human cytokine rec	c 956	20	1.7	31	20	AAQ81234	Rev-caspase-6 cDNA
884	21	1.8	2882	22	AAQ63424	Human CD39-L2 spli	c 957	20	1.7	35	21	AAQ96242	PCR primer used to
c 885	21	1.8	2952	21	AAQ99029	Human pancreatic c	c 958	20	1.7	36	22	AAQ63653	Plasmid pNCO-SB-H6
c 886	21	1.8	2970	16	AAQ87835	Human neuronal cal	c 959	20	1.7	38	20	AAQ23096	A. thaliana gene a
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ALIGNMENTS

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XX WO200028058-A2.

PD 18-MAY-2000.

XX 09-NOV-1999; 99WO-US26514.

XX 09-NOV-1998; 98US-0107643.

PR 10-NOV-1998; 98US-0107810.

XX (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
 PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;

XX WPI; 2000-376568/32.
 DR P-PSDB; AAY96219.

XX New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

XX Claim 1; Page 86; 94pp; English.

CC The present sequence is the coding sequence of maize leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.

XX Sequence 622 BP; 131 A; 212 C; 164 G; 100 T; 15 other;

Query Match 3.3%; Score 39; DB 21; Length 622;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 tgtgggccatgagccgctcgttcgactacgtcg 411
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 Db 346 tgtgggccatgagccgctcgttcgactacgtcg 384

RESULT 4

AAA27458

ID AAA27458 standard; cDNA; 763 BP.

XX AAA27458;

XX 11-SEP-2000 (first entry)

DE Maize LEC1 # 2 coding sequence.

XX Maize; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KW selectable marker; transgenic plant; transgenic seed; HAP3; ss.

XX Zea mays.

XX Key Location/Qualifiers
 FT CDS 1..483
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FT /product= "Maize LEC1 # 2"
 FT /partial

PN WO200028058-A2.

XX 18-MAY-2000.

XX 09-NOV-1999; 99WO-US26514.

XX 09-NOV-1998; 98US-0107643.

PR 10-NOV-1998; 98US-0107810.

XX (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
 PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;

XX WPI; 2000-376568/32.
 DR P-PSDB; AAY96218.

XX New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

XX Claim 1; Page 84-85; 94pp; English.

CC The present sequence is the coding sequence of maize leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.

XX Sequence 763 BP; 131 A; 255 C; 241 G; 136 T; 0 other;

Query Match 3.3%; Score 39; DB 21; Length 763;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 tgtgggccatgagccgctcgttcgactacgtcg 411
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 Db 35 tgtgggccatgagccgctcgttcgactacgtcg 73

RESULT 5

AAA27460

ID AAA27460 standard; cDNA; 1121 BP.

XX AAA27460;

XX 11-SEP-2000 (first entry)

DE Soybean LEC1 # 2 coding sequence.

XX Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KW selectable marker; transgenic plant; transgenic seed; HAP3; ss.

XX Glycine max.

XX Key Location/Qualifiers
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 FT /partial
 FT /product= "Soybean LEC1 # 2"

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 FT /transl_except= (pos:678..686,aa:Asn)
 FT /transl_except= (pos:726..731,aa:Asp)
 FT /transl_except= (pos:741..746,aa:Gln)
 FT /transl_except= (pos:765..770,aa:Cys)
 FT /transl_except= (pos:783..788,aa:Leu)
 FT /transl_except= (pos:822..827,aa:Ser)
 FT /transl_except= (pos:828..833,aa:Ser)
 FT /transl_except= (pos:930..935,aa:Tyr)
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 FT /transl_except= (pos:1103..1106,aa:Phe)
 FT /note= "Codons have apparent insertions of three
 nucleotides which encode stop codons"
 FT XX
 PN WO200028058-A2.
 XX
 PD 18-MAY-2000.
 XX
 PD 09-NOV-1999; 99WO-US26514.
 XX
 PF 09-NOV-1998; 98US-0107643.
 XX
 PR 10-NOV-1998; 98US-0107810.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
 PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
 XX
 DR WPI: 2000-376568/32.
 DR P-PSDB; AAY96220, AAY96224.
 XX
 PT New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -
 XX
 PS Claim 1: Page 87-89; 94pp; English.
 XX
 CC The present sequence is the coding sequence of soybean leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.
 XX
 SQ Sequence 1121 BP; 324 A; 233 C; 263 G; 301 T; 0 other;

Query Match 2.7%; Score 32; DB 21; Length 1121;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 gagtcgtcgtcggagtagcatcatcagttcatcac 310
 ||||||||||||||||||||||||||||||||
 Db 279 gagtcgtcgtcggagtagcatcatcagttcatcac 310

RESULT 6
 AAA27461
 ID AAA27461 standard; cDNA; 796 BP.
 XX
 AC AAA27461;

XX 11-SEP-2000 (first entry)
 XX
 DE Soybean LEC1 # 3 coding sequence.
 XX
 KW Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KW selectable marker; transgenic plant; transgenic seed; HAP3; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..516
 FT /*tag= a
 FT /product= "Soybean LEC1 # 3"
 FT /partial
 XX
 PN WO200028058-A2.
 XX
 PD 18-MAY-2000.
 XX
 PD 09-NOV-1999; 99WO-US26514.
 XX
 PF 09-NOV-1998; 98US-0107643.
 XX
 PR 10-NOV-1998; 98US-0107810.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Lowe KS, Gordon-Kamm WJ, Klein TM, Rasco-Gaunt S, Cahoon RE;
 PI Sun X, Hoerster GJ, Gregory CA, Nadimpalli R;
 XX
 DR WPI: 2000-376568/32.
 DR P-PSDB; AAY96221.
 XX
 PT New HAP3-type CCAAT-box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -
 XX
 PS Claim 1: Page 90-91; 94pp; English.
 XX
 CC The present sequence is the coding sequence of soybean leafy cotyledon 1
 CC transcriptional activator, LEC1. This sequence encodes a HAP3-type
 CC CCAAT-box binding protein. LEC1 expression initiates the formation of
 CC embryo-like structures and improves growth and recovery of transformants.
 CC When apomixis occurs, i.e. the replacement of sexual reproduction by
 CC asexual reproduction, LEC1 expression in the nucellus integument, or
 CC cell specific expression in the megaspore mother cell would trigger
 CC embryo formation from maternal tissues only. This results in the
 CC production of seeds identical to the parent. Using LEC1, transgenic high
 CC yielding seeds could be developed. In addition, LEC1 could be used for
 CC positive selection of a transformed cell (transgenic plant), for
 CC increasing transformation efficiency and for increasing recovery of
 CC regenerated plants.
 XX
 SQ Sequence 796 BP; 208 A; 174 C; 188 G; 226 T; 0 other;

Query Match 2.2%; Score 26; DB 21; Length 796;
 Best Local Similarity 100.0%; Pred. No. 0.99;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 264 aaggagacgacgagtcgagtcgctgc 289
 ||||||||||||||||||||||||||||
 Db 112 aaggagacgacgacgagtcgctgc 137

RESULT 7
 AAC93983
 ID AAC93983 standard; cDNA; 417 BP.
 XX
 AC AAC93983;
 XX
 DT 19-FEB-2001 (first entry)

```

XX DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:478.
XX DE
XX KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
XX KW flea infestation; vaccine; antiparasitic; therapeutic target;
XX KW diagnosis; detection; ss.
XX OS Ctenocephalides felis.
XX PN WO200061621-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US09437.
XX PR 09-APR-1999; 99US-0128704.
XX PA (HESK-) HESKA CORP.
XX PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX DR WPI; 2000-656323/63.
XX PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic
XX PT acids useful for the prevention, diagnosis and treatment of flea
XX PT infestations.
XX PS Claim 26; Page 403; 964pp; English.
XX CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic
XX CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
XX CC or head and nerve cord (HNC) tissue. The invention also relates to the
XX CC encoded proteins. The invention additionally encompasses expression
XX CC constructs, recombinant viruses and recombinant cells comprising the
XX CC nucleic acids of the invention, recombinant production of the proteins,
XX CC antibodies against the proteins, a method of identifying inhibitors of
XX CC the proteins, and compositions comprising the inhibitors for
XX CC administration to an animal. The nucleic acids, and the proteins they
XX CC encode may be used in the prevention, treatment and diagnosis of diseases
XX CC associated with flea infestations. For example, the nucleic acids may be
XX CC used to produce an HMT or HNC protein according to standard recombinant
XX CC DNA methodology by inserting the nucleic acids into a host cell and
XX CC culturing the cell to express the protein. The HMT and HNC nucleic acids
XX CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
XX CC and quantitate the presence of cat flea or other homologous nucleic acid
XX CC sequences in samples. They may also be used to study the expression and
XX CC function of the proteins and their role in metabolism. The HMT and HNC
XX CC proteins may be used as antigens in the production of specific
XX CC antibodies, and in assays to identify modulators (agonists and
XX CC antagonists) of HMT and/or HNC protein expression and activity. The
XX CC anti-HMT/HNC protein antibodies and antagonists may also be used to
XX CC downregulate protein expression and activity. The antibodies may also be
XX CC used as diagnostic agents for detecting the presence of flea polypeptides
XX CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
XX CC present sequence represents a cat flea HMT cDNA of the invention.
XX SQ Sequence 417 BP; 172 A; 64 C; 63 G; 118 T; 0 other;

Query Match 2.1%; Score 25; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
| | | | | | | | | | | | | | | | | |
Db 391 ttatttcaaaaaaaaaaaaaaaaaa 415

RESULT 8
AAC94808
ID AAC94808 standard; cDNA; 417 BP.
XX
AC AAC94808;

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```

XX DT 19-FEB-2001 (first entry)
XX DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1303.
XX KW Cat flea; hindgut and Malpighian tubule nucleic acid; HMT;
XX KW flea infestation; vaccine; antiparasitic; therapeutic target;
XX KW diagnosis; detection; ss.
XX OS Ctenocephalides felis.
XX PN WO200061621-A2.
XX PD 19-OCT-2000.
XX PF 07-APR-2000; 2000WO-US09437.
XX PR 09-APR-1999; 99US-0128704.
XX PA (HESK-) HESKA CORP.
XX PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;
XX DR WPI; 2000-656323/63.
XX PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic
XX PT acids useful for the prevention, diagnosis and treatment of flea
XX PT infestations.
XX PS Claim 26; Page 665; 964pp; English.
XX CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic
XX CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue
XX CC or head and nerve cord (HNC) tissue. The invention also relates to the
XX CC encoded proteins. The invention additionally encompasses expression
XX CC constructs, recombinant viruses and recombinant cells comprising the
XX CC nucleic acids of the invention, recombinant production of the proteins,
XX CC antibodies against the proteins, a method of identifying inhibitors of
XX CC the proteins, and compositions comprising the inhibitors for
XX CC administration to an animal. The nucleic acids, and the proteins they
XX CC encode may be used in the prevention, treatment and diagnosis of diseases
XX CC associated with flea infestations. For example, the nucleic acids may be
XX CC used to produce an HMT or HNC protein according to standard recombinant
XX CC DNA methodology by inserting the nucleic acids into a host cell and
XX CC culturing the cell to express the protein. The HMT and HNC nucleic acids
XX CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect
XX CC and quantitate the presence of cat flea or other homologous nucleic acid
XX CC sequences in samples. They may also be used to study the expression and
XX CC function of the proteins and their role in metabolism. The HMT and HNC
XX CC proteins may be used as antigens in the production of specific
XX CC antibodies, and in assays to identify modulators (agonists and
XX CC antagonists) of HMT and/or HNC protein expression and activity. The
XX CC anti-HMT/HNC protein antibodies and antagonists may also be used to
XX CC downregulate protein expression and activity. The antibodies may also be
XX CC used as diagnostic agents for detecting the presence of flea polypeptides
XX CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The
XX CC present sequence represents a cat flea HMT cDNA of the invention.
XX SQ Sequence 417 BP; 172 A; 64 C; 63 G; 118 T; 0 other;

Query Match 2.1%; Score 25; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
| | | | | | | | | | | | | | | | | |
Db 391 ttatttcaaaaaaaaaaaaaaaaaa 415

RESULT 9
AAC94808
ID AAC94808 standard; cDNA; 1234 BP.

```


DE Reverse PCR primer used to amplify delta E2.
 XX
 KW Hepatitis C virus; envelope protein E2; hypervariable region 1;
 KW peptide library; treatment; prevent infection; antibody production;
 KW PCR primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9960132-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 14-MAY-1999; 99WO-EP03344.
 XX
 PR 19-MAY-1998; 98GB-0010756.
 XX
 PA (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
 XX
 PI Nicosia A, Lahm A, Tramontano A, Cortese R;
 XX
 XX WPI; 2000-126382/11.
 XX
 PT A new peptide library from hepatitis C virus, useful for production of
 PT treatment for hepatitis C -
 XX
 XX Example 6; Page 80; 126pp; English.
 XX
 CC This sequence represents a PCR primer used to amplify delta E2, the gene
 CC encoding an envelope protein of Hepatitis C virus. The PCR product is
 CC used in the construction of the peptide library of the invention. The
 CC invention relates to a library of peptides which have an immunologically
 CC reactive epitope of the hypervariable region 1 (HVR1) of envelope
 CC protein 2 (E2) of hepatitis C virus. The peptides correspond to formulae
 CC given in the specification (see AAV78596-Y78598). The peptides can be
 CC used in a method to select antibodies which react with the HVR1 of E2 of
 CC hepatitis C virus, through the selection of those antibodies which bind
 CC to the peptides. The peptides from hepatitis C virus hypervariable region
 CC 1 of the envelope protein E2 are used to produce a medicament for raising
 CC or increasing levels of antibodies able to bind HCV (hepatitis C virus)
 CC HVR1 epitopes in a mammal. The medicament is used to treat or prevent an
 CC HCV infection.
 XX
 SQ Sequence 36 BP; 3 A; 5 C; 17 G; 11 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 36;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 ctaccgcaccaccaccaccaccac 602
 ||||||||||||||||||||
 Db 36 CTACCGCACCACCACCACCACCAC 13

RESULT 12
 AAV73459
 ID AAV73459 standard; cDNA: 500 BP.
 XX
 AC AAV73459;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Flea saliva protein nucleic acid nfspL3-500.
 XX
 KW Flea saliva protein; nfspL3-500; allergic dermatitis; allergen;
 KW allergy; therapy; diagnosis; vaccine; ectoparasite; ss.
 XX
 OS Ctenocephalides sp.
 XX
 XX KEY Location/Qualifiers
 FH CDS 1..186
 FT /*tag- a
 FT
 XX

PN WO9845408-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 15-OCT-1997; 97WO-US18669.
 XX
 PR 10-APR-1997; 97WO-US05959.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Weber ER;
 XX
 DR WPI; 1998-594480/50.
 DR P-PSDB; AAW82393.
 XX
 PT New isolated ectoparasite saliva genes - used to develop products
 PT for the diagnosis, prevention, treatment and determining
 PT susceptibility to allergic dermatitis
 XX
 PS Claim 1; Page 157; 172pp; English.
 XX
 CC This is the nucleotide sequence of nfspL3-500, which encodes a
 CC non-full-length flea salivary protein, termed pfspL3-61 (see
 CC AAW82393). The clone was obtained by PCR amplification (see
 CC AAV73455-58) from a whole flea cDNA library. Its sequence shows no
 CC significant homology to known sequences. A DNA probe based on
 CC nfspM(N)880 may be useful for isolating the full-length clone.
 CC The invention is directed to methods for isolating ectoparasite
 CC saliva proteins (ESPs), including flea saliva proteins. It
 CC provides ESPs (claimed, see AAW82382-93), nucleic acid molecules
 CC encoding them, methods for their recombinant production,
 CC therapeutic compositions for treating allergic dermatitis that
 CC comprise at least one ESP, as well as assay kits for testing if an
 CC animal has, or is susceptible to, allergic dermatitis, and a method
 CC of desensitising a host animal to allergic dermatitis using ESPs.
 CC The ESPs can also be used for the production of antibodies useful
 CC in diagnosis or in vaccines for passive immunisation against
 CC allergic dermatitis.
 XX
 SQ Sequence 500 BP; 230 A; 62 C; 58 G; 150 T; 0 other;

Query Match 2.0%; Score 24; DB 19; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaa 1171
 ||||||||||||||||||||
 Db 477 attatttcaaaaaaaaaaaaaa 500

RESULT 13
 AAV73460/C
 ID AAV73460 standard; cDNA: 500 BP.
 XX
 AC AAV73460;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Flea saliva protein nucleic acid nfspL3-500 (complement).
 XX
 KW Flea saliva protein; nfspL3-500; allergic dermatitis; allergen;
 KW allergy; therapy; diagnosis; vaccine; ectoparasite; ss.
 XX
 OS Ctenocephalides sp.
 XX
 PN WO9845408-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 15-OCT-1997; 97WO-US18669.
 XX
 PR 10-APR-1997; 97WO-US05959.

XX PA (HESK-) HESKA CORP.
 XX PI Weber ER;
 XX XX
 DR WPI; 1998-594480/50.
 XX
 XX New isolated ectoparasite saliva genes - used to develop products
 PT for the diagnosis, prevention, treatment and determining
 PT susceptibility to allergic dermatitis
 XX
 PS Claim 1; Page 158; 172pp; English.
 XX
 CC This is the nucleotide sequence of nucleic acid nfpSL3-500
 CC complementary strand. The coding strand (see AAV73459) encodes a
 CC non-full-length flea salivary protein, termed PfslpL3-61 (see
 CC AW82293). The clone was obtained by PCR amplification (see
 CC AAV73455-58) from a whole flea cDNA library. Its sequence shows no
 CC significant homology to known sequences. A DNA probe based on
 CC nfpSM(N)880 may be useful for isolating the full-length clone.
 CC The invention is directed to methods for isolating ectoparasite
 CC saliva proteins (ESPs), including flea saliva proteins. It
 CC provides ESPs (claimed, see AAW82382-93), nucleic acid molecules
 CC encoding them, methods for their recombinant production,
 CC therapeutic compositions for treating allergic dermatitis that
 CC comprise at least one ESP, as well as assay kits for testing if an
 CC animal has, or is susceptible to, allergic dermatitis, and a method
 CC of desensitising a host animal to allergic dermatitis using ESPs.
 CC The ESPs can also be used for the production of antibodies useful
 CC in diagnosis or in vaccines for passive immunisation against
 CC allergic dermatitis.
 XX
 SQ Sequence 500 BP; 150 A; 58 C; 62 G; 230 T; 0 other;

Query Match 2.0%; Score 24; DB 19; Length 500;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaa 1171
 |||||||||||||||||||
 Db 24 ATTATTTCAAAAAAAAAAAAAA 1

RESULT 14
 AAH87686/c
 ID AAH87686 standard; cDNA; 653 BP.
 AC AAH87686;
 XX
 XX 25-SEP-2001 (first entry)
 DT
 DE Peppermint plant oil gland expressed cDNA 42.
 XX
 XX Peppermint; plant oil gland cell; terpenoid essential oil; resin;
 KW genetic mapping; antisense suppression; recombinant expression; ss.
 XX
 XX Mentha x piperita.
 OS
 XX WO200153319-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 19-JAN-2001; 2001WO-US02567.
 XX
 XX 20-JAN-2000; 2000US-0177264.
 PR
 XX (CROT/) CROTEAU R B.
 PA (LANG/) LANGE B M.
 PA (WILD/) WILDUNG M R.
 XX
 XX Croteau RB, Lange BM, Wildung MR;
 PI
 XX

DR WPI; 2001-488706/53.
 XX
 XX New nucleic acid molecules corresponding to mRNA molecules expressed in
 PT peppermint oil glands for enhancing expression of plant oil gland cell
 PT proteins -
 XX
 PS Claim 1; Page 93; 251pp; English.
 XX
 CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
 CC correspond to all or part of a mRNA molecule expressed in plant oil
 CC gland cells, especially peppermint and plant oil glands that produce
 CC terpenoid essential oils and resins. The nucleic acids are useful for
 CC genetically mapping a plant genome for genes expressed in plant oil
 CC gland cells and to suppress (for example by antisense suppression) or
 CC enhance their expression (for example by genetically transforming a
 CC plant cell with a replicable expression vector that expresses one or more
 CC proteins naturally expressed in plant oil gland cells). The nucleic acids
 CC are also useful for recombinant expression of plant oil gland proteins
 CC required for terpenoid essential oil and/or resin production in bacterial
 CC and/or yeast cells.
 XX
 SQ Sequence 653 BP; 165 A; 150 C; 134 G; 202 T; 2 other;

Query Match 2.0%; Score 24; DB 22; Length 653;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
 |||||||||||||||||||
 Db 28 TATTTCAAAAAAAAAAAAAA 5

RESULT 15
 AAA59457
 ID AAA59457 standard; DNA; 886 BP.
 XX
 AC AAA59457;
 XX
 XX 14-NOV-2000 (first entry)
 DT
 DE Nucleotide sequence of a soybean type I glutathione-S-transferase.
 XX
 KW Soybean; glutathione-S-transferase; GST; detoxification;
 KW xenobiotic compound; herbicide-tolerance; transgenic plant;
 KW herbicide synergist; ss.
 XX
 OS Glycine max.
 XX
 XX Key Location/Qualifiers
 FH CDS 18..623
 FT /*tag= a
 FT /product= "glutathione-S-transferase"
 XX
 XX WO200047728-A2.
 PN
 XX 17-AUG-2000.
 PD
 XX 10-FEB-2000; 2000WO-US03347.
 PF
 XX 10-FEB-1999; 99US-0247373.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX McGonigle B, O'Keefe DP;
 PI
 XX WPI; 2000-549144/50.
 DR P-PSDB; AAB07826.
 XX
 XX Soybean glutathione-S-transferase polypeptides and polynucleotides used
 PT to produce herbicide tolerant transgenic plants and to screen for
 PT inhibitors or substrates of the enzyme -
 XX

PS Claim 2; Page 55; 84pp; English.

XX The present sequence encodes a soybean glutathione-S-transferase
CC (GST) enzyme. The enzyme is involved in the detoxification of
CC xenobiotic compounds in plants and seeds. The GST polynucleotides
CC and polypeptides are used for the production of herbicide-tolerant
CC transgenic plants, and for the development of screening assays to
CC identify GST inhibitors and substrates, which can be used as
CC herbicide synergists. GST gene specific probes can be used in gene
CC identification methods. The recombinant GST enzymes can be used to
CC produce enzyme specific antibodies which are used to detect the
CC enzymes in situ in cells or in vitro in cell extracts.

XX SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886

RESULT 16

AAZ53393
ID AAZ53393 standard; cDNA; 886 BP.

AC AAZ53393;

XX 04-OCT-2000 (first entry)

XX Clone se.127b04 nucleotide sequence encoding GST type I.

XX Soybean; glutathione-S-transferase; GST; detoxify; herbicide; stress;
KW transgenic plant; tolerant; plant breeding; ss.

XX Glycine max.

XX US063570-A.

XX 16-MAY-2000.

XX 05-SEP-1997; 97US-0924747.

XX 05-SEP-1997; 97US-0924747.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX McGonigle B, O'Keefe DP;

XX WPI: 2000-375487/32.

XX P-PSDB; AAB03731.

XX New Glutathione-S-Transferase enzymes and isolated nucleic acid
PT fragments encoding them, useful for detoxifying xenobiotic compounds in
PT plants and seeds, as well as in producing transgenic plants that are
PT herbicide-resistant

XX Claim 2; Column 25-26; 36pp; English.

XX This sequence was isolated from a soybean clone, and encodes a
CC Glutathione-S-Transferase (GST). The invention relates to isolated
CC nucleic acid fragments (see AAZ53393-A53406) which encode soybean GST
CC polypeptides (AAB03731-B03744). GSTs are a family of enzymes which
CC catalyze the conjugation of glutathione, homogluthathione and other
CC glutathione-like analogues, to a large range of hydrophobic,
CC electrophilic compounds. GSTs have been implicated in the detoxification
CC of certain herbicides. The GST nucleotide sequences are useful in the
CC construction of herbicide-tolerant transgenic plants, plants that are
CC tolerant to a wide variety of stresses, or plants in which the GST
CC enzymes are present at higher or lower levels than they are normally.

CC The nucleic acid fragments are also useful as probes for genetically and
CC physically mapping the genes that they are part of, and as markers for
CC traits linked to expression of the enzymes. This will be useful in plant
CC breeding in order to develop lines with desired phenotypes or in the
CC identification of mutants. The soybean GST enzymes are used to detoxify
CC xenobiotic compounds in plants and seeds. The enzymes are also useful as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that may be used as herbicides or herbicide synergists. The GST enzymes
CC produced in the host cells, particularly in microbial host cells, are
CC useful in preparing antibodies to the enzymes. These antibodies are
CC useful for detecting the enzymes in situ in cells or in vitro in cell
CC extracts.

XX SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886

RESULT 17

AAZ94949

ID AAZ94949 standard; cDNA; 886 BP.

XX AAZ94949;

XX 01-AUG-2000 (first entry)

XX Soybean glutathione-S-transferase cDNA clone sel.27B04.

XX Soybean; glutathione-S-transferase; GST; xenobiotic;
KW detoxification; transgenic plant; herbicide tolerance; ss.

XX Glycine max.

XX Key Location/Qualifiers
FT CDS 18..623
FT /*tag= a

FT /EC_number= 2.5.1.18

XX WO200018936-A1.

XX 06-APR-2000.

XX 30-SEP-1998; 98WO-US20501.

XX 30-SEP-1998; 98WO-US20501.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX McGonigle B, O'Keefe DP;

XX WPI: 2000-317517/27.

XX P-PSDB; AAY79512.

XX Nucleic acids encoding soybean glutathione-S-transferase enzymes useful
PT for conferring herbicide resistance to plants

XX Claim 2; Page 39; 76pp; English.

XX The present sequence is that of the cDNA insert in clone
CC sel.27B04 encoding soybean class I glutathione-S-transferase
CC (GST, see AAY79512). The clone was isolated from a cDNA library
CC prepared from soybean embryo. The invention provides soybean GST
CC enzymes (see AAY79512-25) involved in the detoxification of
CC xenobiotic compounds, especially herbicides, in plants and seeds.
CC Chimeric genes encoding all or a portion of soybean GST enzymes,
CC host cells, and methods of recombinant production of soybean GST

CC enzymes are provided. The sequences are useful in the construction
 CC of herbicide-tolerant transgenic plants, in the recombinant
 CC production of GST enzymes, in the development of screening assays
 CC to identify compounds inhibitory to the GST enzymes (useful as
 CC herbicides or herbicide synergists), and in screening assays to
 CC identify chemical substrates of the GSTs.

SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 886;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 ||||||||||||||||||||
 Db 863 tatttcaaaaaaaaaaaaaaaaaa 886

RESULT 18

AAF31572
 ID AAF31572 standard; DNA; 886 BP.

XX AC AAF31572;

DT 09-APR-2001 (first entry)

DE Soybean type I GST cDNA.

XX Soybean; glutathione-S-transferase; herbicide; GST; ds.

XX Glycine max.

XX US6171839-B1.

XX 09-JAN-2001.

XX 22-APR-1999; 99US-0296715.

XX 05-SEP-1997; 97US-0924747.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX McGonigle B, O'Keefe DP;

XX WPI; 2001-136874/14.

XX Novel soybean glutathione-S-transferase enzymes useful as targets to
 PT facilitate design and/or identification of inhibitors of the enzyme,
 PT that are used as herbicides or herbicide synergists -

XX Claim 2; Column 25-26; 37pp; English.

CC The present invention relates to soybean glutathione-S-transferase
 CC proteins. The novel sequences are useful in the construction of
 CC herbicide tolerant transgenic plants, in the recombinant production
 CC of glutathione-S-transferase (GST) enzymes, in the development of
 CC screening assays to identify compounds inhibitory to the GST enzymes,
 CC and in screening assays to identify chemical substrates of the GSTs.

SQ Sequence 886 BP; 250 A; 166 C; 199 G; 271 T; 0 other;

Query Match 2.0%; Score 24; DB 22; Length 886;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 ||||||||||||||||||||
 Db 863 tatttcaaaaaaaaaaaaaaaaaa 886

RESULT 19

AAZ52292
 ID AAZ52292 standard; cDNA; 1231 BP.

XX AC AAZ52292;

DT 18-JUL-2000 (first entry)

DE Maize replication protein A middle subunit homologue-7 (ZmRPAMSH7) cDNA.

XX Maize; Replication protein A; RPA; middle subunit; ZmRPAMSH; virucide;
 KW fungicide; insecticide; chromosome 5; DNA-binding protein; DNA repair;
 KW DNA metabolism; DNA replication; cell cycle; homologous recombination;
 KW pathogen resistance; fungi; virus; nematode; insect; gene therapy;
 KW genetic manipulation; ss.

XX Zea mays.

XX Key Location/Qualifiers

XX CDS 85..514

XX /*tag= a

XX /product= "Maize replication protein A middle subunit
 FT homologue-7"

XX /note= "Mapped to chromosome 5"

XX WO200015816-A2.

XX 23-MAR-2000.

XX 15-SEP-1999; 99WO-US21277.

XX 17-SEP-1998; 98US-0100690.

XX 11-MAR-1999; 99US-0123896.

XX (PION-) PIONEER HI-BRED INT INC.

XX Mahajan P;

XX WPI; 2000-271452/23.

XX P-PSDB; AAY70710.

XX New maize replication protein A useful for genetic transformation, gene
 PT targeting in plants and modulating DNA metabolism -

XX Claim 2c; Page 98-100; 101pp; English.

XX The present sequence is a cDNA encoding the maize replication protein A
 CC (RPA) middle subunit homologue-7 (ZmRPAMSH7). RPA is a single-stranded
 CC DNA-binding protein required for multiple processes in DNA metabolism,
 CC like DNA replication, repair mechanism (e.g. nucleotide excision and
 CC double stranded (ds) DNA break repair) and recombination. The gene
 CC for the ZmRPAMS homologue is mapped to chromosome 5. This sequence
 CC has fungicide, virucide and insecticidal activity. DNA encoding RPA is
 CC used for modulating DNA metabolism, influencing cell cycle, enhancing
 CC homologous recombination and increasing pathogen resistance in plants.
 CC Pests that can be controlled include fungal pathogens, viruses,
 CC nematodes and insects. Antisense sequences can be used to block RPA
 CC expression and promote non-specific recombination events. RPA protein
 CC can be used to improve genetic manipulation and also in gene therapy.

XX Sequence 1231 BP; 338 A; 296 C; 303 G; 294 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 1231;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173

Db 1196 tatttcaaaaaaaaaaaaaaaaaa 1219

RESULT 20
 AAF55043

ID	AAF55043 standard; DNA; 1316 BP.
XX	
AC	AAF55043;
XX	
DT	15-MAY-2001 (first entry)
XX	
DE	Nucleotide sequence of a calcium channel transport polypeptide.
XX	
KW	Calcium channel transport polypeptide; calcium trafficking;
KW	neural disorder; HIV-induced dementia; immune system disorder;
KW	rheumatoid arthritis; muscular disorder; muscle contractile dysfunction;
KW	reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW	cardiovascular disorder; arrhythmia; renal disorder;
KX	proliferative disorder; cancer; lung carcinoma; breast cancer; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 36..341
FT	/tag= a
FT	/product= "calcium channel transport polypeptide"
XX	
PN	WO200108635-A2.
XX	
PD	08-FEB-2001.
XX	
PF	27-JUL-2000; 2000WO-US20392.
XX	
PR	28-JUL-1999; 99US-0145958.
PR	18-AUG-1999; 99US-0149446.
PR	14-MAR-2000; 2000US-0189064.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Ni J, Shi Y;
XX	
DR	WPI: 2001-138604/14.
DR	P-PSDB; AAB67466.
XX	
PT	New isolated nucleic acid useful for diagnosing, detecting, or treating
PT	or preventing diseases associated with anomalies in calcium trafficking
PT	across the plasma membrane -
XX	
PS	Claim 1; Page 254; 259pp; English.
XX	
CC	The present sequence encodes a calcium channel transport polypeptide.
CC	The polynucleotides, polypeptides, and antibodies are useful for
CC	preventing, treating, or ameliorating diseases associated with anomalies
CC	in calcium trafficking across the plasma membrane. They are used to
CC	diagnose, detect and treat or prevent diseases or conditions such as
CC	neural disorders (e.g. HIV-induced dementia), immune system disorders
CC	(e.g. rheumatoid arthritis), muscular disorders (e.g. muscle contractile
CC	dysfunction), reproductive disorders, gastrointestinal disorders,
CC	pulmonary disorders, cardiovascular disorders (e.g. arrhythmias), renal
CC	disorders, proliferative disorders, and/or cancerous diseases and
CC	conditions (e.g. lung carcinoma or breast cancer).
XX	
SQ	Sequence 1316 BP; 458 A; 227 C; 237 G; 394 T; 0 other;
Query Match 2.0%; Score 24; DB 22; Length 1316;	
Best Local Similarity 100.0%; Pred No. 4, 7;	
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1150 tatttcacaaaaaaaaaaaaaa 1173
Db	1291 tatttcacaaaaaaaaaaaaaa 1314
RESULT	21
AAH24830	
ID	AAH24830 standard; DNA; 1372 BP.
XX	

XX Cuticlin; gene therapy; vaccine; helminth parasite; ss.
 KW
 XX
 OS

XX Dirofilaria immitis.
 XX
 PN

XX US6248329-B1.
 XX
 PD

XX 19-JUN-2001.
 XX
 PF

XX 01-JUN-1999; 9905-0323427.
 XX
 PD

XX 01-JUN-1998; 9805-0087435.
 XX
 PF

XX (CHAN/) CHANDRASHEKAR R.
 XX
 PD

XX (MORA/) MORALES T H.
 XX
 PD

XX Chandrashekar R, Morales TH;
 XX
 PD

XX WPI; 2001-396953/42.
 XX
 PD

XX Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin
 PT protein is useful as a vaccine to prevent parasitic helminth infection
 PT

XX Example 1; Column 43-46; 29pp; English.
 XX
 PS

XX The specification describes a Dirofilaria immitis nucleic acid molecule,
 CC that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid
 CC molecule is useful as a probe to identify nucleic acid molecules, as a
 CC primer to produce nucleic acids, as a therapeutic reagent, e.g., gene
 CC therapy to inhibit cuticlin activity or production, or in a vaccine to
 CC prevent infection with helminth parasites. The cuticlin protein,
 CC antibodies raised against it, and inhibitory compounds of cuticlin may
 CC all be used in compositions to protect animals, especially mammals such
 CC as cats, dogs, and humans. The antibodies may be used to passively
 CC immunize an animal, or as reagents in assay to detect infection of
 CC helminths, or as tools to screen expression libraries to recover desired
 CC proteins. They may also be used to target cytotoxic agents to the
 CC parasite and kill it directly. The present sequence represents the
 CC complement of DNA encoding a cuticlin polypeptide.
 XX

SQ Sequence 1372 BP; 406 A; 281 C; 229 G; 456 T; 0 other;

Query Match 2.0%; Score 24; DB 22; Length 1372;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1150 tatttcaaaaaaiaaaaaaaaaa 1173

DB 32 TATTTCAAAAAIAAAAAAAAAA 9

RESULT 23

AAAF16022

ID AA16022 standard; cDNA; 1399 BP.

XX AA16022;

XX 13-MAR-2001 (first entry)

DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:457.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease; ss.
 XX

OS Homo sapiens.

XX WO200055174-A1.

XX 30-SEP-1999.

XX 21-SEP-2000.
 PD

XX 08-MAR-2000; 2000WO-US05988.
 XX

XX 12-MAR-1999; 9905-0124270.
 XX

XX (HUMA-) HUMAN GENOME SCI INC.
 XX

XX (ROSE/) ROSEN C A.
 XX

XX Rosen CA, Ruben SM;
 XX

XX WPI; 2000-587513/55.
 XX

XX P-PSDB; AAB56819.
 XX

XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -

XX Claim 1; Page 934; 2338pp; English.

XX AA15566 to AA16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AA16506 to AA16514 to
 CC AA57303 represent sequences used in the exemplification of the present
 CC invention.
 XX

SQ Sequence 1399 BP; 302 A; 402 C; 389 G; 303 T; 3 other;

Query Match 2.0%; Score 24; DB 21; Length 1399;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1150 tatttcaaaaaaiaaaaaaaaaa 1173

DB 1344 tatttcaaaaaaiaaaaaaaaaa 1367

RESULT 24

AAZ25133

ID AA225133 standard; cDNA; 1466 BP.

XX AA225133;

XX 13-DEC-1999 (first entry)

DE Human hypoxia induced gene HIG2 cDNA sequence.

XX Hypoxia induced gene; HIG; cancer; ischaemia; diagnosis; reperfusion;
 KW retinopathy; neonatal distress; pre-eclampsia; cardiac arrest; stroke;
 KW stress; hypoxia; ionising radiation; hypothermia; heat shock; ss.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 274..465

XX /*Tag= a

XX /product= "HIG2"

XX WO9948916-A2.

XX 30-SEP-1999.

PF 29-MAR-1999; 99WO-US06860.
XX
PR 27-MAR-1998; 98US-0049719.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA (STRI) SRI INT.
XX
XX Denko NC, Giaccia AJ, Green CJ, Laderoute KR, Schindler C;
PI Koong AC;
XX
XX WPI; 1999-580418/49.
DR P-PSDB; AAY42135.
XX
XX New isolated hypoxia-inducible genes, used to develop products for
PT diagnosis and treatment of hypoxia-related conditions, e.g. cancer,
PT ischaemia, reperfusion, retinopathy, neonatal distress, pre-eclampsia,
PT cardiac arrest or stroke -
XX
XX Claim 1; Fig 2; 109pp; English.
XX
XX The present sequence represents the human hypoxia-inducible gene HIG2.
CC Methods from the present invention can be used for identifying genes
CC inducible or repressible by stress, e.g. hypoxia, ionizing radiation,
CC hypothermia or heat shock. They can also be used for the diagnosis and
CC treatment of hypoxia related conditions e.g. cancer, ischaemia,
CC reperfusion, retinopathy, neonatal distress, pre-eclampsia, cardiac
CC arrest, or stroke,
XX
XX Sequence 1466 BP; 345 A; 357 C; 392 G; 372 T; 0 other;

Query Match 2.0%; Score 24; DB 20; Length 1466;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
Db 1417 tatttcaaaaaaaaaaaaaaaaaa 1440

RESULT 25
AAD03429
ID AAD03429 standard; cDNA; 1466 BP.
XX
AC AAD03429;
XX
DT 13-JUN-2001 (first entry)
XX
DE Human hypoxia-inducible gene, HIG2 cDNA.
XX
KW Human; hypoxia-inducible gene; HIG1; HIG2; antiischaemic; preeclampsia;
KW cytosolic; cerebroprotective; cardiac; ophthalmological; retinopathy;
KW reperfusion; neonatal distress; cardiac arrest; stroke; wound healing;
KW cancer; ischaemia; drug screening; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 274..465
FT /tag= a
FT /product= "Human HIG2 protein"
XX
XX WO200123426-A2.
XX
XX 05-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US27189.
XX
XX 30-SEP-1999; 98US-0410375.
XX
XX (VARI) VARIAN ASSOC INC.
XX
XX Denko NC, Giaccia AJ, Green CJ, Laderoute KR, Schindler C;
PI

PI Koong AC;
XX
DR WPI; 2001-226926/23.
DR P-PSDB; AAE00286.
XX
XX New assays, useful for determining the presence of hypoxia and for
PT evaluating a hypoxia-related condition in an animal, comprises
PT hypoxia-inducible genes, hypoxia-inducible polypeptides (HIP) or
PT antibodies immunoreactive with HIP -
XX
XX Example 3; Fig 2A; 110pp; English.
XX
XX The present cDNA sequence encodes human hypoxia-inducible protein, HIG2.
CC The invention relates to human hypoxia-inducible genes (HIG) such as
CC HIG1, HIG2, and their corresponding protein molecules. HIG proteins are
CC useful for treating hypoxia-related conditions such as ischaemia,
CC reperfusion, retinopathy, neonatal distress, preeclampsia, cardiac
CC arrest, cardiac stroke, wound healing and cancer, by attenuating the
CC hypoxic response of a tissue in an animal such as human. Protein
CC expression products of HIG are useful for diagnosing and screening drugs
CC for the treatment of hypoxia-related conditions. Immunoreactive HIG
CC antibodies are useful for isolating HIG1 and HIG2 from cells or
CC biological fluids. The invention also relates to methods for assaying the
CC expression of HIG, for determining the presence of hypoxia and for
CC evaluating the hypoxia-related condition. Methods are also provided for
CC identifying the stress-inducible and stress-repressible genes.
XX
XX Sequence 1466 BP; 345 A; 357 C; 392 G; 372 T; 0 other;

Query Match 2.0%; Score 24; DB 22; Length 1466;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
Db 1417 tatttcaaaaaaaaaaaaaaaaaa 1440

RESULT 26
AAD09829
ID AAD09829 standard; cDNA; 1928 BP.
XX
AC AAD09829;
XX
DT 12-SEP-2001 (first entry)
XX
DE Soybean SPF1-related transcription factor #5 cDNA.
XX
KW Soybean; SPF1-related transcription factor; transgenic plant;
KW genetical mapping; physical mapping; plant breeding; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 12..1739
FT /tag= a
FT /product= "SPF1-related transcription factor #5"
XX
XX WO200149840-A2.
XX
XX 12-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35310.
XX
XX 04-JAN-2000; 2000US-0174325.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Zhu Q, Famodu OO, Rafalski JA;
XX
XX WPI; 2001-441876/47.
XX
XX P-PSDB; AAE05092.

XX Novel isolated SPFI-1 related transcription factor polypeptides and
 PT polynucleotides useful for producing transgenic plants -
 XX
 XX Claim 7: Page 52-53; 60pp; English.
 XX
 CC The present sequence is soybean SPFI-related transcription factor #5
 CC cDNA. The SPFI-related transcription factor is useful for transforming a
 CC cell by introducing SPFI-related transcription factor into a cell. It is
 CC also useful for producing a transgenic plant by transforming a plant cell
 CC with SPFI-related transcription factor and regenerating a plant from the
 CC transformed plant cell. It is also useful to create transgenic plants in
 CC which SPFI-related transcription factor DNA is present at higher or lower
 CC levels than normal or in cell types or developmental stages in which they
 CC are not normally found. The SPFI-related transcription factor DNA is
 CC useful to prepare antibodies. It is also used as probes for genetically
 CC and physically mapping the genes that they are a part of, and used as
 CC markers for traits linked to these genes. Such information is useful in
 CC plant breeding in order to develop lines with desired phenotype.
 XX
 SQ Sequence 1928 BP; 591 A; 454 C; 387 G; 496 T; 0 other;

Query Match 2.0%; Score 24; DB 22; Length 1928;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaaa 1173
 |||||
 Db 1905 tatttcaaaaaaaaaaaaaaa 1928

RESULT 27
 AAC59457
 ID AAC59457 standard; cDNA; 2254 BP.
 XX
 AC AAC59457;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human secreted protein gene 9 SEQ ID NO:19.
 XX
 KW Human; secreted protein; diagnosis; antiarthritic; immunosuppressive;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; nontropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; vulnery; gene therapy; autoimmune disease;
 KW hyperproliferative disorder; neoplasia; cancer; cardiovascular disorder;
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;
 KW infection; ocular disorder; wound healing; skin aging; food additive;
 KW preservative; ss.
 KW
 OS Homo sapiens.
 XX
 PN WO200056755-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 16-MAR-2000; 2000WO-US06830.
 XX
 PR 19-MAR-1999; 99US-0125361.
 PR 10-DEC-1999; 99US-0169910.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 PI WPI: 2000-587661/35.
 DR P-PSDB; AAB34100.
 DR
 XX New isolated nucleic acid molecules encoding 49 human secreted proteins
 FT used for preventing, treating or ameliorating medical conditions, for
 PT diagnosing pathological conditions or as food additives or
 PT preservatives -

XX
 PS Claim 1: Page 336-337; 419pp; English.
 XX
 CC The polynucleotide sequences given in AAC59449 to AAC59497 encode the
 CC human secreted proteins given in AAB34092 to AAB34140. AAB34141 to
 CC AAB34216 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissue
 CC and cells the genes are expressed in. Examples of activities include:
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytostatic; cardiant; vasotropic; cerebroprotective; nontropic;
 CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
 CC and vulnery. The polynucleotides and polypeptides can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms or
 CC cancer of the breast or liver, cardiovascular disorders, cerebrovascular
 CC disorders, angiogenesis, nervous system disorders, infections caused by
 CC bacteria, viruses and fungi and ocular disorders. The polypeptides can
 CC also be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used
 CC as a food additive or preservative to increase or decrease storage
 CC capabilities. AAC59440 to AAC59448 and AAB34091 represent sequences used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 2254 BP; 721 A; 401 C; 410 G; 722 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 2254;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaaa 1173
 |||||
 Db 1791 tatttcaaaaaaaaaaaaaaa 1814

RESULT 28
 AAQ12152
 ID AAQ12152 standard; DNA; 2327 BP.
 XX
 AC AAQ12152;
 XX
 DT 24-SEP-1991 (first entry)
 XX
 DE Human transferrin gene.
 XX
 KW iron-binding protein; clone Tf; liver cDNA library; ss.
 KW Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT sig_peptide 31..87
 FT mat_peptide 88..2124
 FT /tag= a
 FT /tag= b
 FT /product= transferrin
 XX
 PN US5026651-A.
 XX
 PD 25-JUN-1991.
 XX
 PF 25-APR-1985; 85US-0727335.
 XX
 PR 25-APR-1985; 85US-0727335.
 XX
 PA (TEXA) UNIV OF TEXAS SVST.
 XX
 PI Bowman BH, Yang F;

This invention describes novel recombinant human serum transferrin mutants with altered metal binding properties. The products of the invention act as iron chelators. The recombinant transferrins can be used in metal chelation therapy to bind and clear excess toxic metals in patients suffering from metal overloads. In particular transferrin mutants which bind iron with higher avidity than natural transferrin can be administered to individuals suffering from thalassemia to remove excess toxic iron from the body. Half-molecules or transferrin mutants with altered metal ion selectivities could be used to clear other toxic metals e.g. lead, mercury, cadmium copper or zinc from the body. Recombinant full length transferrin can also be used in non serum supplements or in tissue culture media. A transferrin half-molecule is advantageous as it is able to pass through the glomeruli of the kidney and can be excreted in the urine, unlike the holo-proteins, so that the metal is not only chelated but also cleared from the body. The single half-molecules do not bind to transferrin receptors on the membrane of tissue cells and therefore do not deliver the iron to these tissues. A further advantage is that the human body probably recognizes the half-molecules as 'self' and would not elicit an immunological response. Using recombinant transferrin avoids the risk of contamination with HIV or hepatitis virus associated with transferrin purified from human serum. This sequence encodes the human serum transferrin described in the invention.

Sequence 2327 BP; 623 A; 538 C; 627 G; 539 T; 0 other;

Query Match 2.0%; Score 24; DB 21; Length 2327;
Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps
Matches 24; Conservative 0;

QY 1150 tatttcacaaaaaaaaaaaaaa 1173
|||||
DB 2293 tatttcacaaaaaaaaaaaaaa 2316

RESULT 30
AAx76374
ID AAX76374 standard; cDNA; 2993 BP.
AC AAX76374;
XX
DT 05-AUG-1999 (first entry)
DE
PE Pneumocystis carinii isoleucyl-tRNA synthetase encoding cDNA.
KW pneumocystis carinii; lysyl-tRNA synthetase; tyrosyl-tRNA synthetase;
KW aminoacyl-tRNA synthetase; pneumonia; AIDS; immuno-compromised;
KW Acquired Immune Deficiency Syndrome; detection; ds.
XX
OS Pneumocystis carinii.
XX
Key Location/Qualifiers
CDS 1..2937
/*tag= a
XX
US5912140-A.
PN
XX
15-JUN-1999.
XX
03-APR-1995; 95US-0415593.
PD
XX
03-APR-1995; 95US-0415593.
PA
XX
(CUBI-) CUBIST PHARM INC.
PI
XX Pollitis-Virk KI, Quinn CL, Schimmel PR, Tao N, Whoriskey SK;
XX WPI: 1999-357196/30.
DR P-PSDB; AAY17509.
XX
XX Nucleic acids encoding Pneumocystis carinii aminoacyl-tRNA

PT synthetase enzymes useful for detecting similar sequences in samples
 PT and in the study and treatment of pneumonia in Acquired Immune
 PT Deficiency Syndrome patients

XX Disclosure; Column 79-86; 66pp; English.

XX The present sequence encodes Pneumocystis carinii (P. carinii)
 CC isoleucyl-tRNA synthetase, which is an aminoacyl-tRNA synthetase enzyme.
 CC The nucleic acids encoding aminoacyl-tRNA synthetase enzymes may be used
 CC to produce expression vectors and host cells for the recombinant
 CC production of Pneumocystis aminoacyl-tRNA synthetases. The proteins may
 CC then be used in other procedures such as separating amino acids from
 CC samples or as antigens in the production of antibodies. The nucleic
 CC acids may also be used to produce tester cell strains (which contain the
 CC nucleic acids) which may be used to test candidate drugs (e.g. tRNA
 CC synthetase inhibitors) for the treatment of disorder associated with
 CC P. carinii such as pneumonia which is a common complication for Acquired
 CC Immune Deficiency Syndrome (AIDS) patients and other immuno-compromised
 CC individuals. Additionally, they may also be used to detect and isolate
 CC related DNAs in sample (i.e. they can be used as probes).

XX Sequence 2993 BP; 1042 A; 354 C; 561 G; 1036 T; 0 other;

Query Match 2.0%; Score 24; DB 20; Length 2993;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaaaaa 1173
 |||||||
 Db 2963 tatttcaaaaaaaaaaaaaaaaaa 2986

RESULT 31
 AAZ00877/c
 ID AAZ00877 standard; DNA; 24 BP.
 AC AAZ00877;
 XX 27-SEP-1999 (first entry)
 XX PCR primer PGRT32 for PGI coding sequence.
 XX PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
 KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
 KW PSA; human; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9932644-A2.
 PN 01-JUL-1999.
 XX 22-DEC-1998; 98WO-IB02133.
 XX 09-SEP-1998; 98US-0099658.
 PR 22-DEC-1997; 97US-0996306.
 XX (GEST) GENSET.
 XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen D;
 PI WPI; 1999-405178/34.
 DR Use of a prostate cancer associated gene and biallelic markers
 XX derived from it
 XX Example 6; Page 42; 385pp; English.

XX The invention relates to a mammalian PGI gene and protein, and a set of
 CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
 CC used in a hybridisation assay, a sequencing assay, or in an

CC allele-specific amplification assay for determining the identity of a
 CC nucleotide at a PGI-related biallelic marker. The methods can be used to
 CC detect and to assess the risk of developing cancer or prostate cancer.
 CC Early-stage diagnosis of prostate cancer relies on prostate specific
 CC antigen (PSA) dosage. However, the effectiveness of this is limited due
 CC to its inability to discriminate between malignant and non-malignant
 CC affections of the organ. A need exists for both a reliable diagnostic
 CC procedure which would enable early-stage diagnosis, and for preventative
 CC and curative treatments of the disease. The PGI gene can be used for
 CC detection of prostate cancer, and the risk of developing it in the
 CC future, and can also be used to determine therapies for the disease.

XX Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||||
 Db 24 ATTTCAAAAAAAAAAAAAAAAA 2

RESULT 32
 AAQ86155/c
 ID AAQ86155 standard; DNA; 42 BP.
 XX AAQ86155;
 AC AAQ86155;
 XX 21-NOV-1995 (first entry)
 XX Sindbis polyA primer.
 DE Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplifi;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX Synthetic.
 OS WO9507994-A.
 PN 23-MAR-1995.
 PD 15-SEP-1994; 94WO-US10469.
 PF 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 XX (VIAG-) VIAGENE INC.
 XX Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 PI Polo JM;
 XX WPI; 1995-131362/17.
 DR New alpha virus vectors for gene therapy - of viral infection,
 PT cancer, auto-immune disease, etc., and as vaccines.
 XX Example 1; Page 58; 260pp; English.

XX The sequences given in AAQ86155-66 are primers which were used in the
 CC cloning of Sindbis genomic length cDNA for inclusion in a eukaryotic
 CC layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's
 CC comprise a 5' sequence capable of initiating transcription of an
 CC alphavirus, a nucleotide sequence encoding alphavirus non-structural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the
 CC viral junction region prevents transcription of the subgenomic
 CC fragment making vectors such as this suitable for a wide variety of
 CC applications, eg. gene therapy for the treatment of cystic fibrosis.

XX SQ Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCACAAAAAAAAAAAAA 19

RESULT 35
AAT35054/C
ID AAT35054 standard; cDNA; 42 BP.

XX AAT35054;
XX 24-FEB-1997 (first entry)
XX Sindbis virus strain AR-339 primer.

XX HSV; herpes simplex virus; solid tumour; killing; cancer; metastasis;
KW neovascularisation; angiogenesis; blood clot; neoplasia; viral vector;
KW gene therapy; ss.

XX Synthetic.

XX W09621416-A2.

XX 18-JUL-1996.

XX 22-DEC-1995; 95WO-US16855.

XX 30-DEC-1994; 94US-0368574.

XX (CHIR) CHIRON VIAGENE INC.

XX Burrows FJ, Dubensky TW, Fong TC, Jolly DJ, Polo JM;

XX WPI; 1996-342012/34.

XX Transducing cells in or adjacent to a tumour with a gene delivery
PT vehicle - useful to kill cells in vivo, inhibit tumour
PT angiogenesis, etc.

XX Example 1; Page 40; 159pp; English.

XX AAT35054 is a PCR primer used to amplify genomic length Sindbis cDNA
CC which is used in the construction of a Sindbis viral vector. The
CC vector may be used to transduce cells in or adjacent to a tumour
CC to inhibit tumour cell growth. The vector may express a protein
CC capable of killing tumour cells by activating a non-cytotoxic agent
CC into a cytotoxic one (e.g. herpes simplex virus (HSV)-1 thymidine
CC kinase). Such a vector can be used to transduce cells of a blood
CC vessel in or adjacent to an arterial side of a tumour. The invention
CC includes other viral vectors expressing other tumour-killing or
CC inhibiting agents, e.g. blood clotting factors (cut off the tumours
CC blood supply), angiogenesis inhibitors (inhibit vascularisation of
CC the tumour) and proteins that render nutrients in the perivascular
CC space of a tumour unusable (by binding to or metabolising the
CC nutrients).

XX SQ Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCACAAAAAAAAAAAAA 19

RESULT 34

AAT30789/C

ID AAT30789 standard; DNA; 42 BP.

XX AAT30789;

XX 12-SEP-1996 (first entry)

XX Sindbis genomic cDNA primer 4B.

XX Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
KW primer; polymerase chain reaction; PCR; ss.

XX Synthetic.

XX W09617072-A2.

XX 06-JUN-1996.

XX 30-NOV-1995; 95WO-US15490.

XX 15-MAR-1995; 95US-0405827.

XX 30-NOV-1994; 94US-0348472.

XX 18-JAN-1995; 95US-0376184.

XX (CHIR) CHIRON VIAGENE INC.

XX Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

XX Jolly DJ, Polo JM;

XX WPI; 1996-277785/28.

XX New recombinant alpha-virus vectors - used to develop prods and
PT methods for use in gene therapy and in the prodn. of vaccines

XX Example 1; Page 59; 256pp; English.

XX An oligonucleotide primer (AAT30789) contains at its 5' end a
CC buffer sequence for efficient restriction endonuclease digestion,
CC a XhoI site, 25 nt nucleotides, and 6 nucleotides that are
CC precisely complementary to the extreme 3' end (nts 11698-11703)
CC of Sindbis virus. It was used for first strand cDNA synthesis from
CC polyA mRNA obtd. from virions of Sindbis virus strain Ar-338 (ATCC
CC VR 1248) propagated in BHK cells. It was also used for the PCR
CC amplification of Sindbis genomic cDNA (see also AAT30790-800) to
CC produce cDNA clone pVSP6GEN useful for vector construction (see
CC also AAT30787).

XX SQ Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 42;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaa 1173

Db 41 ATTTCACAAAAAAAAAAAAA 19

RESULT 35

AAV60127/C

ID AAV60127 standard; DNA; 42 BP.

XX AAV60127;

XX 04-DEC-1998 (first entry)

XX PCR primer 4B used to produce Sindbis virus cDNA.

KW Eukaryotic layered vector initiation system; stimulate; immune response;
 KW PCR primer; ss.

OS Synthetic.
 OS Sindbis virus.

XX US5814482-A.
 XX PN

XX 29-SEP-1998.
 XX PD

XX 30-OCT-1996; 96US-07391158.
 XX PF

XX 15-SEP-1993; 93US-0122791.
 XX PR

XX 18-FEB-1994; 94US-0198450.
 XX PR

XX 14-SEP-1994; 94WO-US10469.
 XX PR

XX 30-NOV-1994; 94US-0348472.
 XX PR

XX 18-JAN-1995; 95US-0376184.
 XX PR

XX 30-OCT-1996; 96US-07391158.
 XX PA

XX (DRIV/) DRIVER D A.
 XX PA

XX (DUBE/) DUBENSKY T W.
 XX PA

XX (JOLLY) JOLLY D J.
 XX PA

XX (POLO/) POLO J M.
 XX PI

XX Driver DA, Dubensky TW, Jolly DJ, Polo JM;
 XX PI

XX WPT; 1998-541753/46.
 XX DR

XX Eukaryotic layered vector initiation system - containing eukaryotic
 XX PT promoter and heterologous antigen coding sequence, useful for
 XX PT stimulating immune response

XX Example 1; Column 51; 144pp; English.
 XX PS

XX PCR primers AAV60127-38 were used to produce and amplify Sindbis
 CC cDNA. This is then used to produce an eukaryotic layered vector
 CC initiation system. The eukaryotic layered vector initiation
 CC system comprises a eukaryotic promoter 5' of viral cDNA which
 CC initiates, in a susceptible target cell, 5' to 3' synthesis of
 CC RNA from the viral cDNA. The RNA comprises a vector construct which
 CC autonomously amplifies in the cell and expresses a heterologous nucleic
 CC acid sequence which encodes an antigen or modified form that stimulates
 CC an immune response within an animal. The system is useful for
 CC stimulating an immune response to an antigen by introducing the vector
 CC into target cells, preferably by infection in vivo, especially where the
 CC immune response is a cell mediated, HLA class I-restricted or an HLA
 CC class II-restricted immune response.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;
 XX SQ

Query Match 2.0%; Score 23; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||

Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 36
 AAV42366/c

ID AAV42366 standard; DNA; 42 BP.
 XX

XX AAV42366;
 XX AC

XX 02-OCT-1998 (first entry)
 XX DT

XX PCR primer 4B used to amplify Sindbis cDNA.
 XX DE

XX DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.

XX KW

OS Synthetic.
 OS Sindbis virus.

XX US5789245-A.
 XX PN

XX 04-AUG-1998.
 XX PD

XX 30-OCT-1996; 96US-0741881.
 XX PF

XX 15-MAR-1995; 95US-0404796.
 XX PR

XX 15-SEP-1993; 93US-0122791.
 XX PR

XX 18-FEB-1994; 94US-0198450.
 XX PR

XX 30-NOV-1994; 94US-0348472.
 XX PR

XX 20-JAN-1995; 95US-0376184.
 XX PR

XX 30-OCT-1996; 96US-0741881.
 XX PA

XX (CHIR) CHIRON CORP.
 XX PI

XX Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 XX PI Polo JM,

XX WPI; 1998-446089/38.
 XX DR

XX DNA alpha:virus structural protein expression cassettes - for
 XX PT producing recombinant alpha:virus particles

XX Example 1; Column 52; 140pp; English.
 XX PS

XX PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and
 CC an alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the
 CC cell, the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;
 XX SQ

Query Match 2.0%; Score 23; DB 19; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||

Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 37
 AAV70686/c

ID AAV70686 standard; DNA; 42 BP.
 XX

XX AAV70686;
 XX AC

XX 02-FEB-1999 (first entry)
 XX DT

XX Primer 4B used to produce Sindbis virus cDNA from mRNA.
 XX DE

XX Alphavirus vector construct; gene therapy; primer; ss.
 KW

XX Synthetic.
 OS

XX Sindbis virus.
 XX OS

XX US5843723-A.
 XX PN

XX 01-DEC-1998.
 XX PD

XX 30-OCT-1996; 96US-0739167.
 XX PF

XX 20-MAR-1995; 95US-0404796.
 XX PR

PR 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 PR 30-NOV-1994; 94US-0348472.
 PR 20-JAN-1995; 95US-0376184.
 PR 30-OCT-1996; 96US-0739167.

XX (CHIR) CHIRON CORP.

XX Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
 PI Jolly DJ, Polo JM;

XX WPI; 1999-044581/04.

XX Alphavirus vectors constructs containing a 5' promoter of viral cDNA
 PT by in vitro transcription - used in gene therapy

XX Example 1; Column 52; 140pp; English.

XX The present primer was used to produce Sindbis virus cDNA from
 CC mRNA. The Sindbis cDNA was then amplified to produce a
 CC genomic length Sindbis cDNA sequence, which was then used to create
 CC the alphavirus vector constructs of the invention. These constructs
 CC comprise a promoter 5' of viral cDNA which initiates the synthesis
 CC of RNA from the viral cDNA by in vitro transcription, followed by
 CC a 5' sequence which initiates transcription of alphavirus RNA,
 CC followed by a nucleotide sequence encoding alphavirus nonstructural
 CC proteins, a viral junction region which has been inactivated such that
 CC viral transcription of a subgenomic fragment is prevented, an internal
 CC ribosome entry site or a sequence which promotes ribosome read through
 CC between adjacent reading frames, and an alphavirus RNA polymerase
 CC recognition sequence. The recombinant alphavirus vectors can be used
 CC for gene therapy.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 38
 AAZ92767/c
 ID AAZ92767 standard; DNA; 42 BP.

XX AC AAZ92767;

XX DT 22-MAY-2000 (first entry)

XX Sindbis virus genomic cDNA PCR primer SEQ ID NO:3.

XX Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
 KW eukaryotic layered vector initiation system; antimicrobial; cardiant;
 KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;
 KW infection; melanoma; cancer; diabetes; diabetes; autoimmune disorder;
 KW graft versus host disease; Alzheimer's disease; heart disease;
 KW haemophilia; cystic fibrosis; PCR primer; ss.

XX Sindbis virus.

XX US6015686-A.

XX PD 18-JAN-2000.

XX PF 15-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

XX PR 18-FEB-1994; 94US-0198450.

XX PR 30-NOV-1994; 94US-0348472.

PR 20-JAN-1995; 95US-0376184.

XX (CHIR) CHIRON VIAGENE INC.

XX Polo JM, Jolly DJ, Driver DA, Dubensky TW;

XX WPI; 2000-181143/16.

XX Eukaryotic layered vector initiation system useful for gene therapy and
 PT production of recombinant protein, comprises promoter that directs
 PT synthesis of RNA containing a vector construct -

XX Example 1; Column 51; 141pp; English.

XX The present invention describes a eukaryotic layered vector initiation
 CC system (A) comprising a eukaryotic promoter (EP), 5' of viral cDNA (I)
 CC which initiates the 5' to 3' synthesis of RNA (II) from (I). (II)
 CC comprises a vector construct (VC), expressing a heterologous nucleic
 CC acid (III), which amplifies autonomously in a cell. (A) can have
 CC anticancer, antiviral, antimicrobial, antidiabetic, immunomodulatory,
 CC antineurodegeneration and cardiant activities. (A) are used to express
 CC therapeutic proteins in cell cultures; in gene therapy (for humans or
 CC animals), e.g. to induce a specific immune response; to inhibit
 CC interaction of an agent with cellular receptors; to express a toxin;
 CC to regulate the immune system or to express a replacement gene, e.g.
 CC for treatment or prevention of infections (by viruses or other
 CC pathogens), melanoma (or other cancers), diabetes (or other autoimmune
 CC disorders), graft versus host disease, Alzheimer's disease, heart
 CC disease, haemophilia, cystic fibrosis and many others; or for production
 CC of packaged vector particles (also useful for gene therapy). (A) can
 CC also be used to produce transgenic plants that express resistance or
 CC growth promoting sequences. AAZ92765 to AAZ92891 and AAZ80146 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 |||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 39
 AAZ92894/c
 ID AAZ92894 standard; DNA; 42 BP.

XX AC AAZ92894;

XX DT 22-MAY-2000 (first entry)

XX Sindbis virus genomic cDNA PCR primer SEQ ID NO:3.

XX Recombinant alphavirus vector; gene therapy; anticancer; antiviral;
 KW eukaryotic layered vector initiation system; antimicrobial; cardiant;
 KW antidiabetic; antineurodegeneration; immunomodulatory; immune response;
 KW infection; melanoma; cancer; diabetes; diabetes; autoimmune disorder;
 KW graft versus host disease; Alzheimer's disease; heart disease;
 KW haemophilia; cystic fibrosis; PCR primer; ss.

XX Sindbis virus.

XX US6015694-A.

XX PD 18-JAN-2000.

XX PF 16-SEP-1997; 97US-0931869.

XX PR 15-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

XX PR 18-FEB-1994; 94US-0198450.

PR 30-NOV-1994; 94US-0348472.
 PR 18-JAN-1995; 95US-0376184.
 PA (CHIR) CHIRON CORP.
 PI Jolly DJ, Chang SM, Polo JM, Dubensky TW;
 XX WPI; 2000-181146/16.
 DR
 XX
 XX Stimulating an immune response in an animal, useful e.g. for protecting
 PT against viruses or tumors, by infecting target cells with recombinant
 PT alphavirus particles that express an antigen -
 XX
 XX Example 1; Column 52; 140pp; English.
 PS
 XX The present invention describes a method for stimulating, in an animal,
 CC an immune response to an antigen (Ag). The method comprises infecting
 CC target cells in the animal with recombinant alphavirus particles (AVP)
 CC that direct expression of at least one Ag, optionally modified, in the
 CC infected cells. AVP are derived from an alphavirus packaging cell line
 CC comprising a stably transformed expression cassette (EC) which expresses
 CC an alphavirus structural protein that is able, after introduction of an
 CC alphavirus vector construct (AVC), to produce recombinant AVP or the
 CC AVPs are free from recombinant AVPs that can initiate productive
 CC infection to produce infectious AVPs. The method is used, in human or
 CC veterinary medicine, to induce an immune response, particularly
 CC cell-mediated or HLA (human leucocyte antigen) Class I or II restricted,
 CC e.g. against viruses (especially hepatitis C), tumours, bacteria,
 CC parasites or fungi. Cells infected with alphavirus particles are fully
 CC viable and present antigens efficiently; the antigenic epitopes exposed
 CC can be altered by selective cloning of gene subfragments (including
 CC expression of multiple epitopes), and they effectively stimulate
 CC cytotoxic T cells. AA292892 to AA293018 and AA290147 represent sequences
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 42 BP; 7 A; 1 C; 3 G; 31 T; 0 other;
 SQ

Query Match 2.0%; Score 23; DB 21; Length 42;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 attcagaaagaaagaaagaaagaa 1173
 Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 40
 AAQ86183/c
 ID AAQ86183 standard; DNA; 48 BP.
 XX
 AC AAQ86183;
 XX
 XX 23-NOV-1995 (first entry)
 DE
 DE Primer SINXball700R amplifies plasmid DNA sindbis basic vector.
 XX
 XX Eukaryotic layered vector initiation system: Sindbis; alphavirus; PCR;
 KW transcription initiation; non-structural protein; subgenomic fragment;
 KW RNA polymerase recognition sequence; ELVIS; gene therapy; amplify;
 KW primer; polymerase chain reaction; cystic fibrosis; ss.
 XX
 OS Synthetic.
 XX
 XX WO9507994-A.
 PN
 XX 23-MAR-1995.
 PD
 XX 15-SEP-1994; 94WO-US10469.
 PF
 XX 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 XX

PA (VIAG-) VIAGENE INC.
 XX
 PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 PI Polo JM;
 XX
 XX WPI; 1995-131362/17.
 DR
 XX
 XX New alpha virus vectors for gene therapy - of viral infection,
 PT cancer, auto-immune disease, etc., and as vaccines.
 PT
 XX Example 3; Page 74; 260pp; English.
 PS
 XX The sequences given in AAQ86182-85 are primers which were used in the
 CC generation of plasmid DNA sindbis basic vectors. The amplified DNA
 CC sequences were used in the construction of a eukaryotic layered vector
 CC initiation system (ELVIS) derived from Sindbis. ELVIS's comprise a 5'
 CC sequence capable of initiating transcription of an alphavirus, a
 CC nucleotide sequence encoding alphavirus non-structural proteins, a
 CC viral junction region which has been inactivated such that viral
 CC transcription of the subgenomic fragment is prevented, and an
 CC alphavirus RNA polymerase recognition sequence. Inactivation of the
 CC viral junction region prevents transcription of the subgenomic
 CC fragment making vectors such as this suitable for a wide variety of
 CC applications, eg. gene therapy for the treatment of cystic fibrosis.
 XX
 XX Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;
 SQ

Query Match 2.0%; Score 23; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 attcagaaagaaagaaagaaagaa 1173
 Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 41
 AAT35073/c
 ID AAT35073 standard; cDNA; 48 BP.
 XX
 AC AAT35073;
 XX
 XX 24-FEB-1997 (first entry)
 DT
 DE Sindbis-based, tumour inhibiting, viral vector construction primer.
 DE
 XX HSV; herpes simplex virus; solid tumour; killing; cancer; metastasis;
 KW neovascularisation; angiogenesis; blood clot; neoplasia; viral vector;
 KW gene therapy; ss.
 XX
 OS Synthetic.
 XX
 XX WO9621416-A2.
 PN
 XX 18-JUL-1996.
 PD
 XX 22-DEC-1995; 95WO-US16855.
 PF
 XX 30-DEC-1994; 94US-0368574.
 PR
 XX (CHIR) CHIRON VIAGENE INC.
 PA
 XX Burrows FJ, Dubensky TW, Fong TC, Jolly DJ, Polo JM;
 PI WPI; 1996-342012/34.
 DR
 XX Transducing cells in or adjacent to a tumour with a gene delivery
 PT vehicle - useful to kill cells in vivo, inhibit tumour
 PT angiogenesis, etc.
 XX
 XX Example 1; Page 50; 159pp; English.
 PS
 XX

CC AAT35072-T35075 are PCR primers used in the construction of Sindbis-
 CC based viral vectors which can be used to transduce cells in or adjacent
 CC to a tumour to inhibit tumour cell growth. The vectors express a
 CC protein capable of killing tumour cells by activating a non-cytotoxic
 CC agent into a cytotoxic one (e.g. herpes simplex virus (HSV)-1 thymidine
 CC kinase). Such a vector can be used to transduce cells of a blood vessel
 CC in or adjacent to an arterial side of a tumour. The invention includes
 CC other viral vectors expressing other tumour-killing or inhibiting
 CC agents, e.g. blood clotting factors (cut off the tumours blood supply),
 CC angiogenesis inhibitors (inhibit vascularisation of the tumour) and
 CC proteins that render nutrients in the perivascular space of a tumour
 CC unusable (by binding to or metabolising the nutrients).
 XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 ||||||||||||||||||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 42
 AAT30807/C
 ID AAT30807 standard; DNA; 48 BP.
 XX
 AC AAT30807;
 XX
 DT 12-SEP-1996 (first entry)
 XX
 DE Sindbis PCR primer SINSac11700R.
 XX
 KW Alphavirus; Sindbis virus; vector; gene therapy; vaccine;
 KW primer; polymerase chain reaction; PCR; PKSSINBV; ss.
 XX
 OS Synthetic.
 XX
 PN WO9617072-A2.
 XX
 PD 06-JUN-1996.
 XX
 PF 30-NOV-1995; 95WO-U515490.
 XX
 PR 15-MAR-1995; 95US-0405827.
 PR 30-NOV-1994; 94US-0348472.
 PR 18-JAN-1995; 95US-0376184.
 XX
 PA (CHIR) CHIRON VIAGENE INC.
 XX
 PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;
 PI Jolly DJ, Polo JM;
 XX
 DR WPI; 1996-277785/28.
 XX
 PT New recombinant alpha-virus vectors - used to develop prods and
 PT methods for use in gene therapy and in the prodn. of vaccines
 XX
 PS Example 3; Page 68; 256pp; English.
 XX
 CC Reverse primer SINSac11700R (AAT30807) has a buffer sequence for
 CC efficient restriction endonuclease digestion, a SacI site, and
 CC a sequence complementary to nucleotides 11700-11692 of Sindbis
 CC genomic DNA. It was mixed with forward primer SIN11664F (AAT30806)
 CC and the product was ligated into pKS II+. A plasmid subclone,
 CC pKSII3/SIN, was obtd. that contained the 40 terminal nucleotides of
 CC the viral 3' end and a 25 bp stretch of dA:dt nucleotides. This
 CC was ligated with a subclone contg. Sindbis nucleotides 1-7643 (see
 CC also AAT30808) to create Sindbis basic vector PKSSINBV, useful in the
 CC construction of recombinant vectors useful for gene therapy and
 CC vaccine prodn.

XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;
 Query Match 2.0%; Score 23; DB 17; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 ||||||||||||||||||||
 Db 41 ATTTCAAAAAAAAAAAAAAAAAA 19

RESULT 43
 AAV42384/C
 ID AAV42384 standard; DNA; 48 BP.
 XX
 AC AAV42384;
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Reverse PCR primer SINSac1700R.
 XX
 KW DNA alphavirus; structural protein expression; inhibit; pathogen;
 KW immune response; stimulate; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN US5789245-A.
 XX
 PD 04-AUG-1998.
 XX
 PF 30-OCT-1996; 96US-0741881.
 XX
 PR 15-MAR-1995; 95US-0404796.
 PR 15-SEP-1993; 93US-0122791.
 PR 18-FEB-1994; 94US-0198450.
 PR 30-NOV-1994; 94US-0348472.
 PR 20-JAN-1995; 95US-0376184.
 PR 30-OCT-1996; 96US-0741881.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ;
 PI Polo JM;
 XX
 DR WPI; 1998-446089/38.
 XX
 PT DNA alpha:virus structural protein expression cassettes - for
 PT producing recombinant alpha:virus particles
 XX
 PS Example 3; Column 57; 140pp; English.
 XX
 CC PCR primers AAV42367-420 and AAV42422-54 are used in the course of the
 CC invention. The specification describes a DNA alphavirus structural
 CC protein expression cassette which comprises an inducible promoter and
 CC an alphavirus structural protein gene, where the promoter directs the
 CC expression of the alphavirus structural protein gene upon induction of
 CC the promoter within a cell, and where prior to induction within the
 CC cell, the expression cassette does not express sufficient quantities of
 CC structural proteins to be cytotoxic to a BHK cell containing the
 CC expression cassette. The products may be used to inhibit pathogens and
 CC stimulate an immune response.

XX
 SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 19; Length 48;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
 ||||||||||||||||||||

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 44

AAV70704/c
ID AAV70704 standard; DNA; 48 BP.

XX AC AAV70704;

XX 02-FEB-1999 (first entry)

XX DE Reverse PCR primer SINSac 11700R for Sindbis virus 3' end.

XX KW Alphavirus vector construct; gene therapy; PCR primer; ss.

XX OS Synthetic.

XX OS Sindbis virus.

XX PN US5843723-A.

XX PD 01-DEC-1998.

XX PF 30-OCT-1996; 96US-0739167.

XX PR 20-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

XX PR 18-FEB-1994; 94US-0198450.

XX PR 30-NOV-1994; 94US-0348472.

XX PR 20-JAN-1995; 95US-0376184.

XX PR 30-OCT-1996; 96US-0739167.

XX PA (CHIR) CHIRON CORP.

XX PI Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

XX PI Jolly DJ, Polo JM;

XX DR WPI; 1999-044581/04.

XX PT Alphavirus vectors constructs containing a 5' promoter of viral cDNA by in vitro transcription - used in gene therapy

XX PS Example 3; Column 57; 140pp; English.

XX CC PCR primers AAV70703-05 are used to amplify the 3' end of Sindbis virus. The amplified product is used in the production of the alphavirus vector constructs of the invention. These constructs comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA from the viral cDNA by in vitro transcription, followed by a 5' sequence which initiates transcription of alphavirus RNA, followed by a nucleotide sequence encoding alphavirus nonstructural proteins, a viral junction region which has been inactivated such that viral transcription of a subgenomic fragment is prevented, an internal ribosome entry site or a sequence which promotes ribosome read through between adjacent reading frames, and an alphavirus RNA polymerase recognition sequence. The recombinant alphavirus vectors can be used for gene therapy.

XX SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 48;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 45

AAZ92785/c

ID AAZ92785 standard; DNA; 48 BP.

XX AC AAZ92785;

XX DT

22-MAY-2000 (first entry)

XX DE Sindbis basic vector construction primer SEQ ID NO:21.

XX KW Recombinant alphavirus vector; gene therapy; anticancer; antiviral; eukaryotic layered vector initiation system; antimicrobial; cardiant; antidiabetic; antineurodegeneration; immunomodulatory; immune response; infection; melanoma; cancer; diabetes; autoimmune disorder; graft versus host disease; Alzheimer's disease; heart disease; haemophilia; cystic fibrosis; PCR primer; ss.

XX OS Sindbis virus.

XX OS Synthetic.

XX PN US6015686-A.

XX PD 18-JAN-2000.

XX PF 15-MAR-1995; 95US-0404796.

XX PR 15-SEP-1993; 93US-0122791.

XX PR 18-FEB-1994; 94US-0198450.

XX PR 30-NOV-1994; 94US-0348472.

XX PR 20-JAN-1995; 95US-0376184.

XX PA (CHIR) CHIRON VIAGENE INC.

XX PI Polo JM, Jolly DJ, Driver DA, Dubensky TW;

XX DR WPI; 2000-181143/16.

XX PT Eukaryotic layered vector initiation system useful for gene therapy and production of recombinant protein, comprises promoter that directs synthesis of RNA containing a vector construct -

XX PS Example 3; Column 57; 141pp; English.

XX CC The present invention describes a eukaryotic layered vector initiation system (A) comprising a eukaryotic promoter (EP), 5' of viral cDNA (I) which initiates the 5' to 3' synthesis of RNA (II) from (I). (II) comprises a vector construct (VC), expressing a heterologous nucleic acid (III), which amplifies autonomously in a cell. (A) can have anticancer, antiviral, antimicrobial, antidiabetic, immunomodulatory, antineurodegeneration and cardiant activities. (A) are used to express therapeutic proteins in cell cultures; in gene therapy (for humans or animals), e.g. to induce a specific immune response; to inhibit interaction of an agent with cellular receptors; to express a toxin; to regulate the immune system or to express a replacement gene, e.g. for treatment or prevention of infections (by viruses or other pathogens), melanoma (or other cancers), diabetes (or other autoimmune disorders), graft versus host disease, Alzheimer's disease, heart disease, haemophilia, cystic fibrosis and many others; or for production of packaged vector particles (also useful for gene therapy). (A) can also be used to produce transgenic plants that express resistance or growth promoting sequences. AAZ92765 to AAZ92891 and AAZ90146 represent sequences used in the exemplification of the present invention.

XX SQ Sequence 48 BP; 10 A; 2 C; 4 G; 32 T; 0 other;

Query Match 2.0%; Score 23; DB 21; Length 48;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 46

AAZ92912/c

ID AAZ92912 standard; DNA; 48 BP.

AA58494/c
ID AAX58494 standard; DNA; 52 BP.

XX AC AAX58494;
XX

DT 16-AUG-1999 (first entry)

XX DE Primer 4B used SIN-1 cDNA PCR.

XX KW SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
KW gene therapy; vaccine; primer; PCR; ss.

XX OS Synthetic.
XX Sindbis virus.

XX PN WO9918226-A2.

XX PD 15-APR-1999.

XX PF 06-OCT-1998; 98WO-US21062.

XX PR 06-OCT-1997; 97US-0944465.

XX PA (CHIR) CHIRON CORP.

XX PI (UNIW) UNIV WASHINGTON.

XX PI Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
PI Schlesinger S;

XX DR WPI; 1999-264032/22.

XX PT Alphavirus vectors with reduced cytopathic effects

XX PS Example 1; Page 103; 235pp; English.

XX CC This primer oligonucleotide, termed 4B, includes an XbaI site, a
CC T35 sequence, and nucleotides 11703-11698 of the Sindbis virus
CC genome. It was used in the PCR amplification of SIN-1 cDNA. A set
CC of primer pairs necessary for amplifying the entire SIN-1 genome is
CC provided (see AAX58483-94). SIN-1 (see AAX58571) is a Sindbis virus
CC variant strain which exhibits reduced inhibition of host
CC macromolecular synthesis and which is capable of establishing
CC persistent infection in vertebrate cells, in contrast to lytic,
CC cytopathogenic wild-type strains of the same virus. The invention
CC relates to alphavirus-based vectors with reduced inhibition of
CC cellular macromolecular synthesis. Alphavirus vector constructs,
CC replicons and eukaryotic layered vector initiation systems are used:
CC (i) to deliver a selected heterologous sequence, particularly in
CC gene therapy for treatment of a wide range of infections, cancers,
CC and autoimmune diseases, or to regulate the immune system; (ii) as
CC vaccines; (iii) to inhibit pathogens; and (iv) to express
CC heterologous products (therapeutic proteins, ribozymes, and
CC antisense sequences). Since the modified vectors do not cause
CC significant inhibition of host cell biosynthesis, they can be used
CC safely as gene therapy vectors.

XX SQ Sequence 52 BP; 7 A; 1 C; 3 G; 41 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

DB 51 ATTTCACAAAAA 29

RESULT 49
AAX59240/c

ID AAX59240 standard; DNA; 58 BP.

XX AC AAX59240;

XX

DT 06-SEP-1999 (first entry)

XX DE Primer 11,703R used in cDNA synthesis from SIN-1 RNA.

XX KW SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
KW gene therapy; vaccine; primer; ss.

XX OS Synthetic.
XX Sindbis virus.

XX PN WO9738087-A2.

XX PD 16-OCT-1997.

XX PF 04-APR-1997; 97WO-US06010.

XX PR 12-JUL-1996; 96US-0679640.

XX PR 05-APR-1996; 96US-0628594.

XX PR 24-JUN-1996; 96US-0668953.

XX PA (CHIR) CHIRON VIAGENE INC.

XX PI (UNIW) UNIV WASHINGTON.

XX PI Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
PI Schlesinger S;

XX DR WPI; 1997-512707/47.

XX PT Nucleic acid comprising altered alpha-virus non-structural protein
PT gene - useful for generating expression cassettes for production of
PT recombinant proteins in vertebrate or insect cells

XX PS Example 1; Page 96; 309pp; English.

XX CC This primer oligonucleotide, termed 11,703R, includes an XhoI site,
CC a dT21 sequence, and nucleotides 11703-11677 of the Sindbis virus
CC genome. It was used in the preparation of first-strand cDNA from
CC genomic RNA isolated from SIN-1 virions. SIN-1 (see AAX59321) is a
CC Sindbis virus variant strain which exhibits reduced inhibition of
CC host macromolecular synthesis and which is capable of establishing
CC persistent infection in vertebrate cells, in contrast to lytic,
CC cytopathogenic wild-type strains of the same virus. The invention
CC relates to alphavirus-based vectors with reduced inhibition of
CC cellular macromolecular synthesis. Alphavirus vector constructs,
CC replicons and eukaryotic layered vector initiation systems are used:
CC (i) to deliver a selected heterologous sequence, particularly in
CC gene therapy for treatment of a wide range of infections, cancers,
CC and autoimmune diseases, or to regulate the immune system; (ii) as
CC vaccines; (iii) to inhibit pathogens; and (iv) to express
CC heterologous products (therapeutic proteins, ribozymes, and
CC antisense sequences). Since the modified vectors do not cause
CC significant inhibition of host cell biosynthesis, they can be used
CC safely as gene therapy vectors.

XX SQ Sequence 58 BP; 13 A; 6 C; 8 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 18; Length 58;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

DB 37 ATTTCACAAAAA 15

RESULT 50
AAX58482/c

ID AAX58482 standard; DNA; 58 BP.

XX AC AAX58482;

DT 16-AUG-1999 (first entry)
XX
DE Primer 11,703R used in cDNA synthesis from SIN-1 RNA.
XX
KW SIN-1; alphavirus; vector; infection; cancer; autoimmune disease;
XX gene therapy; vaccine; primer; ss.
XX
OS Synthetic.
OS Sindbis virus.
XX
PN W09918226-A2.
XX
PD 15-APR-1999.
XX
XX 06-OCT-1998; 98WO-US21062.
XX
XX 06-OCT-1997; 97US-0944465.
PR
XX (CHIR) CHIRON CORP.
PA (UNIW) UNIV WASHINGTON.
XX
XX Belli BA, Dryga SA, Dubensky TW, Frolov I, Polo JM;
PI Schlesinger S;
XX
XX WPI; 1999-264032/22.
DR
XX
XX Alphavirus vectors with reduced cytopathic effects
PT
XX
XX Example 1; Page 100; 235pp; English.
XX
CC This primer oligonucleotide, termed 11,703R, includes an XhoI site,
CC a dt21 sequence, and nucleotides 11703-11677 of the Sindbis virus
CC genome. It was used in the preparation of first-strand cDNA from
CC genomic RNA isolated from SIN-1 virions. SIN-1 (see AX58571) is a
CC Sindbis virus variant strain which exhibits reduced inhibition of
CC host macromolecular synthesis and which is capable of establishing
CC persistent infection in vertebrate cells, in contrast to lytic,
CC cytopathogenic wild-type strains of the same virus. The invention
CC relates to alphavirus-based vectors with reduced inhibition of
CC cellular macromolecular synthesis. Alphavirus vector constructs,
CC replicons and eukaryotic layered vector initiation systems are used:
CC (i) to deliver a selected heterologous sequence, particularly in
CC gene therapy for treatment of a wide range of infections, cancers,
CC and autoimmune diseases, or to regulate the immune system; (ii) as
CC vaccines; (iii) to inhibit pathogens; and (iv) to express
CC heterologous products (therapeutic proteins, ribozymes, and
CC antisense sequences). Since the modified vectors do not cause
CC significant inhibition of host cell biosynthesis, they can be used
CC safely as gene therapy vectors.
XX
SQ Sequence 58 BP; 13 A; 6 C; 8 G; 31 T; 0 other;

Query Match 2.0%; Score 23; DB 20; Length 58;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1151 atttcaaaaaaaaaaaaaaa 1173
Db 37 ATTTCAAAAAAAAAAAAAAAAA 15

Search completed: December 27, 2001, 15:20:28
Job time: 1880 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:49:08 ; Search time 1541.4 Seconds
(without alignments)
8177.500 Million cell updates/sec

Title: US-09-435-054-1
Perfect score: 1173
Sequence: 1 ccacgcgtccgccaccacac.....tcaaaaaaaaaaaaaaaaaa 1173

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 10

Total number of hits satisfying chosen parameters: 7889432

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	7.2	528	10	BE603222 HVSMeh010
2	77	6.6	695	10	AU088581
3	47	4.0	594	10	AL506199 AL506199
4	38	3.2	441	10	AL509098
5	35	3.0	292	11	C28028
6	35	3.0	328	11	C19737
7	27	2.3	368	10	AW670176
8	27	2.3	387	11	BF042068
9	26	2.3	644	10	AV385922
10	26	2.2	67	11	BF013366
11	26	2.2	152	11	BI268661
12	26	2.2	153	11	BG379246

13	26	2.2	177	10	AW356324
14	26	2.2	304	11	BG735393
15	26	2.2	341	11	BG735487
16	26	2.2	342	11	BG603362
17	26	2.2	359	10	AI800247
18	26	2.2	361	11	BG625968
19	26	2.2	379	11	BF411934
20	26	2.2	384	11	BG652352
21	26	2.2	458	10	AW692142
22	26	2.2	458	10	AW790703
23	26	2.2	464	11	BI312519
24	26	2.2	469	10	BI385635
25	26	2.2	472	10	AI380618
26	26	2.2	476	11	BI297090
27	26	2.2	488	10	AI302809
28	26	2.2	490	10	AI588492
29	26	2.2	510	10	AL382797
30	26	2.2	513	10	AI974955
31	26	2.2	530	10	AW066395
32	26	2.2	546	10	AW700042
33	26	2.2	554	10	AW067352
34	26	2.2	584	10	AI450987
35	26	2.2	618	11	BF646151
36	26	2.2	623	13	AZ369897
37	26	2.2	641	11	BF294174
38	26	2.2	683	11	BI094602
39	26	2.2	718	10	AW331967
40	26	2.2	794	10	AW331951
41	26	2.2	100	11	BI151615
42	25	2.1	151	10	AI348819
43	25	2.1	162	10	BE162370
44	25	2.1	174	10	AW424467
45	25	2.1	181	11	BE955607
46	25	2.1	202	10	AL377517
47	25	2.1	218	10	BE760641
48	25	2.1	248	10	AL383797
49	25	2.1	249	11	BG894227
50	25	2.1	275	10	AI619202
51	25	2.1	278	11	BF397037
52	25	2.1	279	11	BG628355
53	25	2.1	280	11	W91845
54	25	2.1	284	10	AI972310
55	25	2.1	286	11	Z21519
56	25	2.1	288	11	BG249632
57	25	2.1	296	11	BF183578
58	25	2.1	300	11	BF301972
59	25	2.1	313	10	AI965374
60	25	2.1	314	10	AA426259
61	25	2.1	316	10	AW620622
62	25	2.1	320	10	AW632871
63	25	2.1	343	11	BF273439
64	25	2.1	344	10	BE318043
65	25	2.1	347	10	AW747449
66	25	2.1	348	10	AI288430
67	25	2.1	350	10	AI204600
68	25	2.1	360	10	AI592230
69	25	2.1	380	10	AV189558
70	25	2.1	383	10	AA901378
71	25	2.1	385	10	AI059972
72	25	2.1	386	11	BG046412
73	25	2.1	392	10	AI301010
74	25	2.1	392	10	AI452746
75	25	2.1	396	10	AI302775
76	25	2.1	397	11	H88112
77	25	2.1	403	11	BI401262
78	25	2.1	405	11	BG373364
79	25	2.1	408	10	AI087244
80	25	2.1	410	11	BG444160
81	25	2.1	417	10	AW589142
82	25	2.1	420	10	AI619296
83	25	2.1	424	10	AA812319
84	25	2.1			
85	25	2.1			

c 86	25	2.1	425	10	AI623732	ts38f03.x	c 159	24	2.0	108	10	AA169635	AA169635	zo94h07.s
c 87	25	2.1	431	11	BE377948	UI-R-CX00-	c 160	24	2.0	148	10	BE014640	BE014640	126444 MA
c 88	25	2.1	431	11	BI294121	UI-R-DK0-	c 161	24	2.0	172	10	BF522452	BF522452	UI-R-C3-U
c 89	25	2.1	432	11	BF277163	GA_Eb002	c 162	24	2.0	173	11	BI284278	BI284278	UI-R-CX09
c 90	25	2.1	433	10	AA879981	vw02f08.f	c 163	24	2.0	176	11	BG349623	BG349623	947031F03
c 91	25	2.1	433	10	AA271535	vd72f06.f	c 164	24	2.0	184	11	BF396055	BF396055	UI-R-B52-
c 92	25	2.1	434	10	AW333719	S25B11 AG	c 165	24	2.0	191	10	AI030368	AI030368	UI-R-C0-J
c 93	25	2.1	435	10	AW761531	s168g10.y	c 166	24	2.0	194	10	AU031968	AU031968	AU031968
c 94	25	2.1	436	10	AW196592	xm35b08.x	c 167	24	2.0	195	10	AI619140	AI619140	486086A01
c 95	25	2.1	436	10	AI682080	tp46007.x	c 168	24	2.0	208	11	BG942050	BG942050	ax20e05.x
c 96	25	2.1	444	10	BE123824	JAYB0070.	c 169	24	2.0	216	10	AL040259	AL040259	DKEF2d434J
c 97	25	2.1	447	10	AW160132	JAYNOA16.	c 170	24	2.0	217	10	AI678285	AI678285	tu80a12.x
c 98	25	2.1	448	10	AI112054	UI-R-YO-m	c 171	24	2.0	217	10	AI885110	AI885110	w189h02.x
c 99	25	2.1	450	11	BG023267	qg39b06.x	c 172	24	2.0	224	10	AI873168	AI873168	wc47e01.x
c 100	25	2.1	451	11	BI347841	d948h01.x	c 173	24	2.0	231	10	AW148355	AW148355	xf13e01.x
c 101	25	2.1	454	11	BI295424	UI-R-DK0-	c 174	24	2.0	240	10	AW026780	AW026780	vv44h08.x
c 102	25	2.1	457	13	AQ224364	HS_2258_B	c 175	24	2.0	242	11	BF458765	BF458765	UI-N-B21-
c 103	25	2.1	459	10	AU100788	AU100788	c 176	24	2.0	248	10	AI696390	AI696390	tw60e10.x
c 104	25	2.1	460	11	BF712183	MI-P-E6-a	c 177	24	2.0	251	10	AL386827	AL386827	MBC37B02
c 105	25	2.1	461	10	AF051125	AF051125	c 178	24	2.0	251	10	AA297325	AA297325	EST112861
c 106	25	2.1	463	11	BG874056	MEST45-G1	c 179	24	2.0	253	10	AW423296	AW423296	sh65g05.y
c 107	25	2.1	466	10	AU077751	AU077751	c 180	24	2.0	255	10	AW458259	AW458259	sh80d10.y
c 108	25	2.1	466	11	BF408506	UI-R-BJ2-	c 181	24	2.0	264	11	BF389206	BF389206	UI-R-B52-
c 109	25	2.1	470	10	AW585203	N211477e	c 182	24	2.0	267	10	AW713411	AW713411	98f07ne.f
c 110	25	2.1	472	10	AL381858	MBC03D08	c 183	24	2.0	276	10	AV240460	AV240460	AV240460
c 111	25	2.1	472	10	AT001659	AT001659	c 184	24	2.0	276	11	BF870582	BF870582	IL3-ET011
c 112	25	2.1	477	11	BF464809	UI-M-CG0P	c 185	24	2.0	279	10	AL512111	AL512111	AL512111
c 113	25	2.1	482	11	BF889899	289509 MA	c 186	24	2.0	285	11	BF458810	BF458810	UI-M-B21-
c 114	25	2.1	488	10	AL373094	MCBAS5F02	c 187	24	2.0	289	10	AA838181	AA838181	oe11f02.s
c 115	25	2.1	494	10	AL501779	AL501779	c 188	24	2.0	290	10	AI274624	AI274624	qv11f08.x
c 116	25	2.1	494	11	BF072624	NCSM3F8T7	c 189	24	2.0	291	11	BE945090	BE945090	UI-M-B20-
c 117	25	2.1	500	10	AI514014	GH27054.3	c 190	24	2.0	291	11	BE991925	BE991925	UI-M-B21-
c 118	25	2.1	510	10	AL385151	MBC26F09	c 191	24	2.0	292	11	C90944	C90944	C90944 D1ct
c 119	25	2.1	512	10	AI751483	cl10c03.y	c 192	24	2.0	293	10	AI641518	AI641518	fc16g01.x
c 120	25	2.1	514	10	AV533740	AV533740	c 193	24	2.0	303	10	AW253664	AW253664	UI-R-BJ0-
c 121	25	2.1	518	10	AW505123	UI-HF-BN0	c 194	24	2.0	307	10	AW657453	AW657453	110669 MA
c 122	25	2.1	523	10	AI733789	606051B09	c 195	24	2.0	314	10	AI844207	AI844207	UI-M-AL1-
c 123	25	2.1	526	11	BG023036	da82908.	c 196	24	2.0	315	10	AW489528	AW489528	UI-M-BH3-
c 124	25	2.1	531	10	AI559017	AEMTBA39	c 197	24	2.0	320	10	AI713661	AI713661	UI-R-AG1-
c 125	25	2.1	535	10	AI884559	wn34c03.x	c 198	24	2.0	322	10	AW291523	AW291523	UI-H-B12-
c 126	25	2.1	537	10	AW332367	S7E8 AGS-	c 199	24	2.0	323	10	AW457172	AW457172	UI-M-BH3-
c 127	25	2.1	540	10	AL501793	AL501793	c 200	24	2.0	329	10	AL381507	AL381507	MBC01D07
c 128	25	2.1	551	10	AA446329	zw67D02.s	c 201	24	2.0	330	10	AL381506	AL381506	MBC01D07
c 129	25	2.1	554	13	BH004117	BMBAC07H1	c 202	24	2.0	333	11	BG631069	BG631069	cc-esflcl
c 130	25	2.1	558	11	BF644533	NF014H04E	c 203	24	2.0	334	10	AI548133	AI548133	UI-R-C3-S
c 131	25	2.1	563	10	AW463485	BP230012B	c 204	24	2.0	334	10	AW522236	AW522236	UI-R-BOO-
c 132	25	2.1	564	10	BF639131	946021C02	c 205	24	2.0	334	10	BE103651	BE103651	UI-R-BX0-
c 133	25	2.1	571	10	AL499965	AL499965	c 206	24	2.0	335	11	R79241	R79241	y188g03.sl
c 134	25	2.1	575	11	BI285870	UI-R-CX0s	c 207	24	2.0	339	10	AI511107	AI511107	UI-R-BT0-
c 135	25	2.1	578	11	C99725	C99725 Rice	c 208	24	2.0	339	10	AW458897	AW458897	sh16c08.y
c 136	25	2.1	581	10	AA986450	uel13d05.x	c 209	24	2.0	340	11	BE993341	BE993341	UI-M-B21-
c 137	25	2.1	608	11	BG300891	HVSMEB001	c 210	24	2.0	340	11	BG058181	BG058181	nah21g05.
c 138	25	2.1	610	10	AU030234	AU030234	c 211	24	2.0	341	11	BF603618	BF603618	269175 MA
c 139	25	2.1	613	10	AW965505	AW965505 EST377593	c 212	24	2.0	342	11	R49579	R49579	y968f10.sl
c 140	25	2.1	614	10	AW139756	UI-H-B11-	c 213	24	2.0	347	13	AZ427469	AZ427469	1M0209L24
c 141	25	2.1	637	11	BG414824	HVSMEX000	c 214	24	2.0	348	10	AI373517	AI373517	qz46f04.x
c 142	25	2.1	639	11	BG415609	HVSMEX000	c 215	24	2.0	348	10	AA190776	AA190776	zp88g01.s
c 143	25	2.1	648	11	BG378168	UI-R-CV1-	c 216	24	2.0	350	10	AU031081	AU031081	AU031081
c 144	25	2.1	668	10	AA218943	zr02h04.s	c 217	24	2.0	353	10	AV661109	AV661109	AV661109
c 145	25	2.1	668	13	AQ508212	RPCI-11-2	c 218	24	2.0	358	10	AA523352	AA523352	n167h05.s
c 146	25	2.1	671	10	AL510350	AL510350	c 219	24	2.0	367	10	AA708908	AA708908	z164a05.s
c 147	25	2.1	698	13	B28405	F18G11TF IG	c 220	24	2.0	369	10	BE097533	BE097533	UI-R-BO1-
c 148	25	2.1	706	11	BI284433	UI-R-CX0s	c 221	24	2.0	374	11	BI042730	BI042730	CM4-OT016
c 149	25	2.1	715	10	AI055045	COBU00020	c 222	24	2.0	375	10	AI087166	AI087166	oz59f11.x
c 150	25	2.1	746	11	BF107484	601823816	c 223	24	2.0	377	10	AU101345	AU101345	AU101345
c 151	25	2.1	769	10	BE033408	ME01C01 M	c 224	24	2.0	377	11	BG631702	BG631702	cc-esflcl
c 152	25	2.1	770	10	AV402769	AV402769	c 225	24	2.0	379	11	BF457952	BF457952	UI-M-B21-
c 153	25	2.1	785	11	BF275540	GA_EB002	c 226	24	2.0	383	11	BF939706	BF939706	cr60h12.x
c 154	25	2.1	791	13	AQ892327	HS_3100_B	c 227	24	2.0	384	11	BE097913	BE097913	UI-R-BX0-
c 155	25	2.1	799	13	AQ889861	HS_3131_A	c 228	24	2.0	385	11	BE939871	BE939871	ax01f10.y
c 156	25	2.1	808	13	B03105	C5RL-167H7-	c 229	24	2.0	386	10	AA528468	AA528468	ne99g07.s
c 157	25	2.1	868	11	BG418528	HVSMEX001	c 230	24	2.0	387	10	AU092049	AU092049	AU092049
c 158	24	2.1	91	10	AI590755	tw18d10.x	c 231	24	2.0	387	10	BE035723	BE035723	MO10A02 M

C 232	24	2.0	388	10	AA960665	ub60d12.s	305	24	2.0	481	10	AA708500	z163a05.s
C 233	24	2.0	388	11	BG627170	cc-esf1cl	306	24	2.0	481	10	AW068737	cn4d03.x
C 234	24	2.0	389	10	AW197753	xx88a10.x	C 307	24	2.0	482	11	B1286328	UI-R-DE0-
C 235	24	2.0	391	10	AI394151	lg60f04.x	C 308	24	2.0	482	13	AQ120372	HS_3010.B
C 236	24	2.0	391	10	AI713766	UI-R-AG1-	C 309	24	2.0	483	11	BF634646	BF634646
C 237	24	2.0	392	11	BI294681	UI-R-DK0-	C 310	24	2.0	486	13	A2823410	2M0097M23
C 238	24	2.0	393	10	AI360437	gy90c09.x	C 311	24	2.0	492	10	A1954489	wk83d02.x
C 239	24	2.0	393	10	AI681040	kx43f09.x	C 312	24	2.0	493	10	A1851735	UI-M-BH0-
C 240	24	2.0	393	11	BG734784	cc-esf1cl	C 313	24	2.0	493	11	N95015	2b45009.s1
C 241	24	2.0	393	11	BI402775	MI-P-CPI-	C 314	24	2.0	497	13	AA550106	AA550106
C 242	24	2.0	394	10	AI705697	UI-R-ADI-	C 315	24	2.0	498	11	BF405603	UI-R-CA1-
C 243	24	2.0	395	10	AI001229	MEST5-A10	C 316	24	2.0	499	10	AL371051	AL371051
C 244	24	2.0	397	11	BG626898	cc-esf1cl	C 317	24	2.0	500	10	A1264147	qk03c06.x
C 245	24	2.0	399	10	AI752996	cr03e05.x	C 318	24	2.0	502	10	AA641019	nr72b09.s
C 246	24	2.0	399	10	AI845108	UI-M-BG0-	C 319	24	2.0	502	10	AL378990	mtb841f1f
C 247	24	2.0	406	11	AI712867	UI-R-AG1-	C 320	24	2.0	506	10	A1622436	486045G06
C 248	24	2.0	406	11	BF596052	su68c02.y	C 321	24	2.0	506	10	AW682891	NF001D12L
C 249	24	2.0	407	10	AI843568	UI-M-AO1-	C 322	24	2.0	506	13	A2060069	RPG1-23-4
C 250	24	2.0	407	10	AW787192	AW787192	C 323	24	2.0	509	11	BI292338	UI-R-DO0-
C 251	24	2.0	407	11	H68635	yr87e12.s1	C 324	24	2.0	510	10	AI059167	UI-R-C1-k
C 252	24	2.0	408	11	BF462451	UI-M-CG0p	C 325	24	2.0	512	11	C96645	C96645
C 253	24	2.0	408	11	BG038801	qg25f11.x	C 326	24	2.0	514	10	AL877404	wm94h03.x
C 254	24	2.0	409	11	AI953784	wx69a03.x	C 327	24	2.0	514	11	BF418559	UI-R-BU2-
C 255	24	2.0	409	11	BG628858	cc-esf1cl	C 328	24	2.0	515	11	BI398611	MI-P-AV1-
C 256	24	2.0	413	11	BI417043	949052D02	C 329	24	2.0	517	11	BF512917	UI-H-BT3-
C 257	24	2.0	417	10	AU102123	AU102123	C 330	24	2.0	518	10	AL369284	MTB830A02
C 258	24	2.0	417	10	AW291816	UI-H-BI2-	C 331	24	2.0	521	10	AI568504	tn40b06.x
C 259	24	2.0	420	11	BG825045	602747506	C 332	24	2.0	522	10	AW007611	wt68a08.x
C 260	24	2.0	421	10	AU002637	UI-R-DO0-	C 333	24	2.0	526	11	T79946	yd85c04.s1
C 261	24	2.0	424	10	AA965089	UI-R-CO-g	C 334	24	2.0	528	10	AL385866	AL385866
C 262	24	2.0	425	10	BE578812	rk02g02.y	C 335	24	2.0	528	13	A2492998	1M0327L19
C 263	24	2.0	426	10	AI079526	qy95h06.x	C 336	24	2.0	530	10	AI767708	wh38h01.x
C 264	24	2.0	428	10	AW434762	AW434762	C 337	24	2.0	530	10	AL383960	MTB818A07
C 265	24	2.0	428	11	BI302732	UI-R-BI0p	C 338	24	2.0	531	10	AW083417	AU083417
C 266	24	2.0	428	11	BF466977	UI-M-CG0p	C 339	24	2.0	534	10	AW410072	fh04a08.y
C 267	24	2.0	428	11	BG664998	1000095D0	C 340	24	2.0	534	11	BG016494	df73b11.x
C 268	24	2.0	431	10	AI548796	UI-R-C3-t	C 341	24	2.0	536	10	AI031539	ow48b03.x
C 269	24	2.0	431	10	AI866390	wk17c03.x	C 342	24	2.0	536	11	BF710159	MI-P-AV1-
C 270	24	2.0	432	11	BG371896	UI-R-CV0-	C 343	24	2.0	540	10	AW489336	UI-M-BH3-
C 271	24	2.0	437	11	BI302741	UI-R-DO0-	C 344	24	2.0	541	10	AW251869	UI-R-BU0-
C 272	24	2.0	441	10	AW298453	UI-H-BW0-	C 345	24	2.0	542	10	BE035563	S48G10.AG
C 273	24	2.0	441	10	AW523860	UI-R-BJ0p	C 346	24	2.0	542	10	BE035563	GA_Ea001
C 274	24	2.0	442	10	AJ273514	AJ273514	C 347	24	2.0	542	11	BI280974	UI-R-DC0-
C 275	24	2.0	443	10	AW492587	UI-M-BH3-	C 348	24	2.0	543	10	AL372114	MTB848F11
C 276	24	2.0	447	11	H05676	yl75f12.s1	C 349	24	2.0	543	11	BF565508	UI-R-BT1-
C 277	24	2.0	448	11	BF457871	UI-M-B21-	C 350	24	2.0	544	10	AW046041	UI-M-BH1-
C 278	24	2.0	449	10	AA97956	NCM2D2T7	C 351	24	2.0	546	10	AI549393	UI-R-C3-u
C 279	24	2.0	453	10	AI741264	wg08e06.x	C 352	24	2.0	547	11	BG529111	602579040
C 280	24	2.0	454	10	AW252481	UI-R-BJ0-	C 353	24	2.0	550	10	BE231408	SS0928.S
C 281	24	2.0	455	10	AW253871	UI-R-BJ0-	C 354	24	2.0	550	11	BE859265	SS0936.S
C 282	24	2.0	455	10	AW529026	UI-R-BT1-	C 355	24	2.0	551	11	BE859265	SS0936.S
C 283	24	2.0	457	10	AU174410	AU174410	C 356	24	2.0	554	11	BE859265	SS0902.S
C 284	24	2.0	458	10	AW293412	UI-H-BI2-	C 357	24	2.0	562	11	BF410374	UI-R-CA1-
C 285	24	2.0	459	11	BF703305	MI-P-A3-a	C 358	24	2.0	564	11	BF403800	UI-R-CA1-
C 286	24	2.0	459	13	AQ218977	HS_2009.A	C 359	24	2.0	564	11	BF407913	UI-R-C3-s
C 287	24	2.0	460	10	AI739036	wi34e05.x	C 360	24	2.0	565	10	BE059973	sn39g06.y
C 288	24	2.0	460	10	AU057459	AW057459	C 361	24	2.0	566	10	AU057653	AU057653
C 289	24	2.0	462	10	AU031947	AU031947	C 362	24	2.0	566	11	BG874166	MEST47-B0
C 290	24	2.0	463	10	AI559217	tu02g04.x	C 363	24	2.0	566	11	BF712786	MI-P-H1-a
C 291	24	2.0	466	10	AU057265	AU057265	C 364	24	2.0	571	10	AW062141	66001D12
C 292	24	2.0	468	10	AI738431	wi23g05.x	C 365	24	2.0	573	11	BI303922	UI-R-DR0-
C 293	24	2.0	471	10	AA748606	ny06a05.s	C 366	24	2.0	577	10	AI738332	606047D06
C 294	24	2.0	472	11	BF419501	UI-R-CA0-	C 367	24	2.0	578	10	AW138879	UI-H-BI1-
C 295	24	2.0	473	10	AW734152	sk80d06.y	C 368	24	2.0	578	10	AW434978	UI-R-BJ0p
C 296	24	2.0	473	10	BE108673	BE108673	C 369	24	2.0	582	11	BG349624	947031F03
C 297	24	2.0	474	10	AW731994	AW731994	C 370	24	2.0	584	10	AA818954	UI-R-A0-a
C 298	24	2.0	474	10	AW731994	AW731994	C 371	24	2.0	586	11	BG938459	cn26c03.y
C 299	24	2.0	474	10	AW699729	gb31c02.y	C 372	24	2.0	587	11	BI270628	NF055B11f
C 300	24	2.0	474	10	AW713456	AW713456	C 373	24	2.0	589	10	AV715534	AV715534
C 301	24	2.0	478	10	AI558276	fb78a12.x	C 374	24	2.0	590	10	AI755132	cr35h02.x
C 302	24	2.0	478	10	BE446185	WHE1142.C	C 375	24	2.0	592	13	AZ859741	2M0165O24
C 303	24	2.0	479	10	BE350119	ht09e07.x	C 376	24	2.0	599	11	BF728377	1000061E1
C 304	24	2.0	480	10	AA190481	zp85e03.s	C 377	24	2.0	601	10	AW255179	ML167 pep

C 378	24	2.0	605	10	AL501906	AL501906	AL501906	C 451	23	2.0	140	10	AI467491
C 379	24	2.0	606	13	B66385	B66385 CIT-HSP-200	B66385 CIT-HSP-200	C 452	23	2.0	141	10	AW485611
C 380	24	2.0	612	11	BE948552	BE948552 UI-M-BH3-	BE948552 UI-M-BH3-	C 453	23	2.0	141	10	BF059386
C 381	24	2.0	617	10	BE580934	BE580934 kp83c10.Y	BE580934 kp83c10.Y	C 454	23	2.0	143	11	AW162554
C 382	24	2.0	617	13	BH005572	BH005572 WBCAC09M2	BH005572 WBCAC09M2	C 455	23	2.0	145	10	AU162554
C 383	24	2.0	624	10	AI691878	AI691878 605011G09	AI691878 605011G09	C 456	23	2.0	146	11	BF225185
C 384	24	2.0	624	10	AI691878	AI691878 605011G09	AI691878 605011G09	C 457	23	2.0	146	11	BF225185
C 385	24	2.0	630	10	AI067182	AI067182 ES2208854	AI067182 ES2208854	C 458	23	2.0	151	10	AI348971
C 386	24	2.0	633	10	AW173527	AW173527 xj08c01.x	AW173527 xj08c01.x	C 459	23	2.0	152	10	AI254067
C 387	24	2.0	635	10	AW509924	AW509924 AV650924	AW509924 AV650924	C 460	23	2.0	152	10	BE155800
C 388	24	2.0	636	10	AL596792	AL596792 DFE2p451J	AL596792 DFE2p451J	C 461	23	2.0	154	11	EG940736
C 389	24	2.0	642	13	A2651906	A2651906 IM0522P21	A2651906 IM0522P21	C 462	23	2.0	156	11	EG940736
C 390	24	2.0	646	13	AW334535	AW334535 S36A11 AG	AW334535 S36A11 AG	C 463	23	2.0	160	10	AA754333
C 391	24	2.0	650	10	AW650865	AW650865 AV650865	AW650865 AV650865	C 464	23	2.0	162	11	EG058871
C 392	24	2.0	655	10	AW162107	AW162107 au73b07.x	AW162107 au73b07.x	C 465	23	2.0	163	10	AW145795
C 393	24	2.0	659	11	BI300991	BI300991 UI-R-DK0-	BI300991 UI-R-DK0-	C 466	23	2.0	166	11	AW155711
C 394	24	2.0	660	11	AW650443	AW650443 AV650443	AW650443 AV650443	C 467	23	2.0	166	11	BF470457
C 395	24	2.0	660	11	AW650443	AW650443 AV650443	AW650443 AV650443	C 468	23	2.0	168	11	EG136794
C 396	24	2.0	668	10	AW711203	AW711203 AV711203	AW711203 AV711203	C 469	23	2.0	168	11	EG136794
C 397	24	2.0	668	10	AW689417	AW689417 NF019A03S	AW689417 NF019A03S	C 470	23	2.0	170	11	BI043033
C 398	24	2.0	671	13	A0404011	A0404011 RPLC1-23-3	A0404011 RPLC1-23-3	C 471	23	2.0	172	11	EG132733
C 399	24	2.0	678	13	A0469180	A0469180 CITBI-EI-	A0469180 CITBI-EI-	C 472	23	2.0	172	11	EG132733
C 400	24	2.0	682	10	AW334058	AW334058 S29H1 AGS	AW334058 S29H1 AGS	C 473	23	2.0	172	11	BF146549
C 401	24	2.0	685	13	AQ308749	AQ308749 CITBI-EI-	AQ308749 CITBI-EI-	C 474	23	2.0	172	11	BF146549
C 402	24	2.0	691	10	AW650877	AW650877 AV650877	AW650877 AV650877	C 475	23	2.0	174	10	AI306203
C 403	24	2.0	708	10	AU097613	AU097613 AU097613	AU097613 AU097613	C 476	23	2.0	174	10	AI306203
C 404	24	2.0	710	10	AW334145	AW334145 S31A11 AG	AW334145 S31A11 AG	C 477	23	2.0	174	11	BE17570
C 405	24	2.0	715	13	AQ317030	AQ317030 CITBI-EI-	AQ317030 CITBI-EI-	C 478	23	2.0	174	11	BE17570
C 406	24	2.0	718	10	BE216256	BE216256 HV-CEB001	BE216256 HV-CEB001	C 479	23	2.0	174	11	BE17570
C 407	24	2.0	719	11	C97610	C97610 C97610 Rice	C97610 C97610 Rice	C 480	23	2.0	176	13	AZ433266
C 408	24	2.0	741	11	BI284285	BI284285 UI-R-CX0S	BI284285 UI-R-CX0S	C 481	23	2.0	177	11	EG509243
C 409	24	2.0	761	11	BF466933	BF466933 UI-M-CG0P	BF466933 UI-M-CG0P	C 482	23	2.0	179	11	BF121471
C 410	24	2.0	766	10	AW652860	AW652860 AV652860	AW652860 AV652860	C 483	23	2.0	180	13	AQ467828
C 411	24	2.0	771	10	AW331991	AW331991 S1E8 AGS-	AW331991 S1E8 AGS-	C 484	23	2.0	183	10	AI010512
C 412	24	2.0	798	13	CNS06N08	AL407238 T7 end of	AL407238 T7 end of	C 485	23	2.0	183	10	AI010512
C 413	24	2.0	801	13	AQ308510	AQ308510 CITBI-EI-	AQ308510 CITBI-EI-	C 486	23	2.0	183	11	BF704134
C 414	24	2.0	809	10	BE564064	BE564064 601348024	BE564064 601348024	C 487	23	2.0	184	11	BE049135
C 415	24	2.0	851	13	AQ750504	AQ750504 HS-5576.B	AQ750504 HS-5576.B	C 488	23	2.0	186	11	EG606807
C 416	24	2.0	877	11	BF663790	BF663790 602145226	BF663790 602145226	C 489	23	2.0	189	11	EG156808
C 417	24	2.0	885	11	BF065790	BF065790 HV-CEB001	BF065790 HV-CEB001	C 490	23	2.0	191	10	AI824801
C 418	24	2.0	1104	10	AU167403	AU167403 AU167403	AU167403 AU167403	C 491	23	2.0	193	10	AL512088
C 419	24	2.0	1369	10	BE421655	BE421655 HWM012CD.	BE421655 HWM012CD.	C 492	23	2.0	193	11	EG509721
C 420	24	2.0	1579	12	AC014727	AC014727 Mus muscu	AC014727 Mus muscu	C 493	23	2.0	196	10	AI445580
C 421	24	2.0	2481	12	BC011742	BC011742 Homo sapi	BC011742 Homo sapi	C 494	23	2.0	197	11	BI135038
C 422	24	2.0	2608	12	AF119843	AF119843 Homo sapi	AF119843 Homo sapi	C 495	23	2.0	198	11	BI042969
C 423	23	2.0	36	10	AW059764	AW059764 LE4C03.Yg	AW059764 LE4C03.Yg	C 496	23	2.0	199	10	AI089462
C 424	23	2.0	60	10	AW409793	AW409793 fh02d08.Y	AW409793 fh02d08.Y	C 497	23	2.0	199	10	AA598553
C 425	23	2.0	63	10	AI340465	AI340465 tq24c11.x	AI340465 tq24c11.x	C 498	23	2.0	200	10	BE216903
C 426	23	2.0	75	10	AW698623	AW698623 g538 gian	AW698623 g538 gian	C 499	23	2.0	200	11	BI268745
C 427	23	2.0	76	11	BI151596	BI151596 nag61h07.	BI151596 nag61h07.	C 500	23	2.0	200	11	BI268745
C 428	23	2.0	90	10	AI246927	AI246927 qx72q02.x	AI246927 qx72q02.x	C 501	23	2.0	200	11	BF408107
C 429	23	2.0	95	10	AI565331	AI565331 t173b06.x	AI565331 t173b06.x	C 502	23	2.0	201	11	BF414859
C 430	23	2.0	98	11	BF579653	BF579653 602093529	BF579653 602093529	C 503	23	2.0	201	10	AI149954
C 431	23	2.0	99	11	BF579266	BF579266 602093437	BF579266 602093437	C 504	23	2.0	205	11	EG630646
C 432	23	2.0	106	10	AA529379	AA529379 v139e11.r	AA529379 v139e11.r	C 505	23	2.0	205	11	F05641
C 433	23	2.0	107	11	AG894048	AG894048 kt17e01.Y	AG894048 kt17e01.Y	C 506	23	2.0	206	11	BF990241
C 434	23	2.0	107	11	BF571999	BF571999 na161e03.	BF571999 na161e03.	C 507	23	2.0	208	11	BF411099
C 435	23	2.0	108	11	BF580150	BF580150 602099159	BF580150 602099159	C 508	23	2.0	209	10	AA432258
C 436	23	2.0	108	11	EG236561	EG236561 na145c04.	EG236561 na145c04.	C 509	23	2.0	212	10	AI491817
C 437	23	2.0	116	11	R26750	R26750 yH44a05.S1	R26750 yH44a05.S1	C 510	23	2.0	214	10	AI036797
C 438	23	2.0	117	10	AI289791	AI289791 qw12c03.x	AI289791 qw12c03.x	C 511	23	2.0	214	10	AI818231
C 439	23	2.0	120	10	AW690406	AW690406 NF032G12S	AW690406 NF032G12S	C 512	23	2.0	214	10	AI825612
C 440	23	2.0	120	11	BF467777	BF467777 UI-M-CG0-	BF467777 UI-M-CG0-	C 513	23	2.0	215	10	AL380992
C 441	23	2.0	121	11	AG090795	AG090795 mac10c04.	AG090795 mac10c04.	C 514	23	2.0	217	10	AI649758
C 442	23	2.0	122	10	AI655445	AI655445 ts98g11.x	AI655445 ts98g11.x	C 515	23	2.0	217	10	AW14918
C 443	23	2.0	122	10	AL047559	AL047559 DFE2p586E	AL047559 DFE2p586E	C 516	23	2.0	217	11	EG455558
C 444	23	2.0	123	10	AI447232	AI447232 mq97h01.x	AI447232 mq97h01.x	C 517	23	2.0	218	11	AL0442529
C 445	23	2.0	127	10	AU161810	AU161810 AU161810	AU161810 AU161810	C 518	23	2.0	218	11	BF044007
C 446	23	2.0	129	10	AW074332	AW074332 xb11c01.x	AW074332 xb11c01.x	C 519	23	2.0	219	11	AW156260
C 447	23	2.0	132	10	AW396329	AW396329 sh03b12.Y	AW396329 sh03b12.Y	C 520	23	2.0	219	11	BI248615
C 448	23	2.0	132	10	AW495627	AW495627 UI-M-BH3-	AW495627 UI-M-BH3-	C 521	23	2.0	220	10	AW237005
C 449	23	2.0	135	10	AI305445	AI305445 qw77c08.x	AI305445 qw77c08.x	C 522	23	2.0	220	10	AW835033
C 450	23	2.0	138	10	AW151446	AW151446 qw77a03.x	AW151446 qw77a03.x	C 523	23	2.0	221	11	BF465396

524	23	2.0	223	11	BI426601	saq05c04.	597	23	2.0	274	10	AW261136	AW261136
525	23	2.0	225	10	AI498683	tm42b04.x	598	23	2.0	274	11	BG625945	BG625945
526	23	2.0	226	10	AI029589	UI-R-C0-i	599	23	2.0	274	11	BF414068	BF414068
527	23	2.0	227	10	AI564350	ts54g04.x	600	23	2.0	276	11	BE147488	BE147488
528	23	2.0	227	10	AW169441	xj26h11.x	601	23	2.0	276	11	BI268819	BI268819
529	23	2.0	228	10	AA386195	EST99973	602	23	2.0	276	11	AI381308	AI381308
530	23	2.0	229	10	AA633592	ac15f07.s	603	23	2.0	277	10	AI550391	AI550391
531	23	2.0	230	11	BG509047	sac93e02.	604	23	2.0	277	10	AL372249	AL372249
532	23	2.0	231	11	BI401566	MI-P-CP0-	605	23	2.0	277	10	AA265736	AA265736
533	23	2.0	231	11	AI590002	tt74f10.x	606	23	2.0	277	10	BE237532	BE237532
534	23	2.0	233	10	AW204438	UI-H-B11-	607	23	2.0	277	11	BF877762	BF877762
535	23	2.0	234	10	AA231147	mw12g01.f	608	23	2.0	278	10	AV726430	AV726430
536	23	2.0	234	10	BE014382	125970.MA	609	23	2.0	278	11	BG626893	BG626893
537	23	2.0	235	10	AI948476	w06c05.x	610	23	2.0	278	11	BF455569	BF455569
538	23	2.0	235	10	AJ410654	AJ410654	611	23	2.0	279	11	BG455755	BG455755
539	23	2.0	235	11	BI275041	UI-R-CX0-	612	23	2.0	279	11	BI275392	BI275392
540	23	2.0	235	11	BI398885	MI-P-AY1-	613	23	2.0	279	11	HI4798	HI4798
541	23	2.0	239	10	AA761284	ni25e07.s	614	23	2.0	280	10	AI752955	AI752955
542	23	2.0	240	10	AU071782	AU071782	615	23	2.0	280	10	AT003712	AT003712
543	23	2.0	240	10	AU073227	AU073227	616	23	2.0	280	11	BG379537	BG379537
544	23	2.0	240	10	AW656769	109200.MA	617	23	2.0	281	11	BG68703	BG68703
545	23	2.0	240	11	BG734762	cc-esf1cl	618	23	2.0	281	11	BF456775	BF456775
546	23	2.0	241	11	BF752269	RG3-BN042	619	23	2.0	282	11	BI276755	BI276755
547	23	2.0	242	11	AA588167	nc23e10.s	620	23	2.0	283	10	BE672357	BE672357
548	23	2.0	243	11	BG735284	cc-esf1cl	621	23	2.0	283	10	AA483300	AA483300
549	23	2.0	244	11	AI095553	q19e11.x	622	23	2.0	284	10	AW125908	AW125908
550	23	2.0	244	11	BG983756	MR4-CN014	623	23	2.0	284	11	BI282440	BI282440
551	23	2.0	244	11	BF426082	sr93f10.y	624	23	2.0	285	10	AW458498	AW458498
552	23	2.0	246	10	AW424733	707064A03	625	23	2.0	286	11	HI8430	HI8430
553	23	2.0	246	11	221558	HSAPIC022.S	626	23	2.0	287	10	AI524414	AI524414
554	23	2.0	247	10	AW512948	x051c05.x	627	23	2.0	287	10	AT003516	AT003516
555	23	2.0	247	11	BG447793	NF069H03E	628	23	2.0	288	11	BF077681	BF077681
556	23	2.0	249	11	BG289244	60238420E	629	23	2.0	288	11	BF548188	BF548188
557	23	2.0	249	11	BE989556	UI-M-BZ1-	630	23	2.0	290	11	BF345645	BF345645
558	23	2.0	250	11	N64249	yz44d10.s1	631	23	2.0	291	10	AU068460	AU068460
559	23	2.0	251	10	AA805063	ob86a12.s	632	23	2.0	291	11	BG629622	BG629622
560	23	2.0	254	10	BE049192	xt73f11.x	633	23	2.0	292	10	AA506744	AA506744
561	23	2.0	255	10	BE552541	946078G08	634	23	2.0	293	10	BE229412	BE229412
562	23	2.0	256	10	AA850564	aml1401.s	635	23	2.0	293	11	BI285753	BI285753
563	23	2.0	258	10	BE058294	sn14c03.y	636	23	2.0	294	10	BE634186	BE634186
564	23	2.0	258	11	BG940516	ax06b02.y	637	23	2.0	294	11	BF419852	BF419852
565	23	2.0	259	10	AW945439	PM0-EN000	638	23	2.0	294	11	BF639061	BF639061
566	23	2.0	259	11	BE233299	139424.MA	639	23	2.0	295	11	D58193	D58193
567	23	2.0	259	11	BI282459	UI-R-DDO-	640	23	2.0	295	13	B66404	B66404
568	23	2.0	260	10	AW043745	wf80h01.x	641	23	2.0	296	10	AA299745	AA299745
569	23	2.0	260	11	BF019319	NF059A12P	642	23	2.0	296	10	AW677806	AW677806
570	23	2.0	261	11	BF019319	uy03g12.y	643	23	2.0	296	11	BG059442	BG059442
571	23	2.0	262	10	AI911623	wc86d01.x	644	23	2.0	297	10	AI184283	AI184283
572	23	2.0	262	10	AW118554	x679f01.x	645	23	2.0	297	11	BG626596	BG626596
573	23	2.0	263	11	BG508359	sac95f04.	646	23	2.0	297	11	BE975579	BE975579
574	23	2.0	265	11	BF403227	UI-R-CAL-	647	23	2.0	298	10	AA836611	AA836611
575	23	2.0	266	10	AI967695	ljlrnpst	648	23	2.0	298	10	AW061804	AW061804
576	23	2.0	266	10	BE750866	202523.MA	649	23	2.0	298	10	AW065734	AW065734
577	23	2.0	266	11	BF993041	IL5-GN017	650	23	2.0	298	10	BE031515	BE031515
578	23	2.0	267	10	AI523094	ar68g10.x	651	23	2.0	298	11	BI264092	BI264092
579	23	2.0	267	10	AU033978	AU033978	652	23	2.0	298	11	BF638105	BF638105
580	23	2.0	268	10	AI261957	qk43b06.x	653	23	2.0	299	11	BF418402	BF418402
581	23	2.0	268	10	AA185667	mu52h03.f	654	23	2.0	300	10	AA371866	AA371866
582	23	2.0	268	11	BG626106	cc-esf1cl	655	23	2.0	300	10	AA514217	AA514217
583	23	2.0	268	11	BI286982	UI-R-CT0S	656	23	2.0	300	11	BG225397	BG225397
584	23	2.0	268	11	BF319154	uy53e09.x	657	23	2.0	302	11	BE996590	BE996590
585	23	2.0	268	11	BF459139	UI-M-BZ1-	658	23	2.0	302	11	BF461501	BF461501
586	23	2.0	269	11	BE233377	139535.MA	659	23	2.0	304	10	BE115846	BE115846
587	23	2.0	270	11	BG628081	cc-esf1cl	660	23	2.0	304	10	BE116207	BE116207
588	23	2.0	270	11	BE986461	UI-M-CG0P	661	23	2.0	304	11	BI291186	BI291186
589	23	2.0	270	13	T02699	0052M7.gmbp	662	23	2.0	305	10	AA836477	AA836477
590	23	2.0	271	10	AA770074	ah72a06.s	663	23	2.0	305	10	AI115675	AI115675
591	23	2.0	271	11	R06542	vf09d09.r1	664	23	2.0	305	10	AL511845	AL511845
592	23	2.0	271	11	BG029045	60222608	665	23	2.0	306	10	AW060637	AW060637
593	23	2.0	272	10	AW473188	xq13b06.x	666	23	2.0	306	11	R23221	R23221
594	23	2.0	272	11	BG943283	ax35q08.x	667	23	2.0	307	10	AW505793	AW505793
595	23	2.0	272	11	BG271853	na16a07.	668	23	2.0	308	10	AA996584	AA996584
596	23	2.0	273	11	BF411265	UI-R-BT1-	669	23	2.0	308	10	AW153019	AW153019

C 670	2.0	308	10	AW192179	x181b03.x	743	2.0	346	10	AU162998	AU162998
C 671	2.0	309	10	AW780454	s171a10.y	744	2.0	346	10	AU597258	vo38a09.r
C 672	2.0	309	11	BF461074	UI-M-CG0p	745	2.0	346	11	BG383630	301814.MA
C 673	2.0	311	10	AI559966	tq77g09.x	746	2.0	346	11	BF751308	RM3-BN042
C 674	2.0	311	10	AI430964	m145f01.x	747	2.0	347	10	AI889943	WM65e01.x
C 675	2.0	313	10	BE024072	sm96d01.y	748	2.0	347	10	AI182023	AU182023
C 676	2.0	313	11	BE996624	UI-M-BZ1-	749	2.0	347	11	BG630213	CC-esf1cL
C 677	2.0	314	11	BG377624	UI-R-CU0-	750	2.0	348	10	AI045405	UI-R-C1-k
C 678	2.0	315	10	AA676604	ad38h09.s	751	2.0	349	10	AI467100	vd65a07.x
C 679	2.0	315	10	AI350489	qt17g02.x	752	2.0	349	10	AL384430	MTBC22A08
C 680	2.0	316	10	AU101900	AU101900	753	2.0	350	10	AU031357	AU031357
C 681	2.0	316	11	BE808365	213641.MA	754	2.0	351	11	BG628565	CC-esf1cL
C 682	2.0	318	10	AA731127	nw68f01.s	755	2.0	352	10	AW090822	xc94c09.x
C 683	2.0	318	13	AQ474700	CTIBI-E1-	756	2.0	352	10	AW691766	AW691766
C 684	2.0	319	10	AA761084	ny13f10.s	757	2.0	352	10	AW959823	EST371894
C 685	2.0	319	10	AI921915	wn86e12.x	758	2.0	354	10	AI853058	UI-M-BHO-
C 686	2.0	319	11	BI013908	KA63-ET020	759	2.0	354	10	AU034731	AU034731
C 687	2.0	320	10	AI463087	u881h01.x	760	2.0	354	11	BF541814	602068486
C 688	2.0	320	10	AW407392	UI-HF-BM0	761	2.0	355	10	AA766825	oa39g05.s
C 689	2.0	320	11	BI297803	UI-R-CV2-	762	2.0	355	10	AW016443	UI-I-B10p
C 690	2.0	322	10	AA733187	zg78g05.s	763	2.0	355	10	AW058281	wx18c05.x
C 691	2.0	322	10	AW503799	UI-HF-BN0	764	2.0	355	11	BI300076	UI-R-CV2-
C 692	2.0	322	10	BE584713	5-5E-Z0.P	765	2.0	355	11	BF418401	UI-R-BJ2-
C 693	2.0	322	11	BF270221	GA_EB000	766	2.0	356	10	AW339279	xz89g06.x
C 694	2.0	323	10	AI383565	tc45e08.x	767	2.0	356	10	BE553897	ur44a02.x
C 695	2.0	323	10	AU066075	AU066075	768	2.0	357	11	BI300059	UI-R-CV2-
C 696	2.0	323	11	BI276625	UI-R-CX0-	769	2.0	357	11	T98458	ye60h01.r1
C 697	2.0	324	10	AI400047	tg90e04.x	770	2.0	358	10	AU032431	AU032431
C 698	2.0	324	10	AU164885	AU164885	771	2.0	358	11	T83606	yd64c03.r1
C 699	2.0	325	10	AW278284	s642b04.y	772	2.0	358	11	BE946474	UI-M-BH3-
C 700	2.0	325	11	BG943273	ax35f08.x	773	2.0	359	10	AI620891	tu85g08.x
C 701	2.0	326	11	BI298061	UI-R-CV2-	774	2.0	360	10	AI873669	wm28c02.x
C 702	2.0	327	10	AI454550	UI-R-BT0-	775	2.0	361	10	AI835429	UI-M-AQ0-
C 703	2.0	327	10	AA534248	nj70g01.s	776	2.0	362	10	AL377097	MTBB29D02
C 704	2.0	327	11	BI135017	UI-M-BH3-	777	2.0	362	10	AW152186	xf75h04.x
C 705	2.0	328	10	AI449664	ma52g03.x	778	2.0	362	10	BE439176	CD01333.W
C 706	2.0	328	11	BG056762	naF9g10.	779	2.0	362	11	BI297407	UI-R-CV2-
C 707	2.0	329	11	BF521936	UI-R-C2p-	780	2.0	363	13	AQ590764	HS_2104.A
C 708	2.0	329	11	AI853332	UI-M-BH0-	781	2.0	364	10	AW761212	nz20c03.s
C 709	2.0	330	10	AW169224	x120f08.x	782	2.0	364	10	AI821603	nc47d01.x
C 710	2.0	331	10	AU101705	AU101705	783	2.0	364	10	AU089779	AU089779
C 711	2.0	332	10	AI010705	AU101705	784	2.0	364	11	AW069375	cr45a07.x
C 712	2.0	333	10	AI547552	UI-R-C3-s	785	2.0	364	11	W78770	zh49e12.r1
C 713	2.0	333	10	AW630479	hh83b12.y	786	2.0	365	10	AA984877	am62c09.s
C 714	2.0	334	10	AA729900	nx40c08.s	787	2.0	365	10	AI791842	nc47d01.y
C 715	2.0	335	10	AI224417	qx11g05.x	788	2.0	365	10	AW081385	xc41f09.x
C 716	2.0	335	10	AI659538	tlul2b05.x	789	2.0	366	10	AA528443	ne84d07.s
C 717	2.0	335	10	AI849698	UI-M-All-	790	2.0	366	11	BG629901	CC-esf1cL
C 718	2.0	335	10	AA512593	vj19a07.r	791	2.0	366	11	BE969598	601679728
C 719	2.0	336	10	AL376831	MTBB26F04	792	2.0	367	10	AI304451	qo54a05.x
C 720	2.0	336	11	BF416379	UI-R-CA0-	793	2.0	368	10	AW072923	xa38b12.x
C 721	2.0	337	10	AA956755	UI-R-E1-f	794	2.0	369	13	AZ754678	cq02f10.f
C 722	2.0	337	10	AI214729	q967c12.x	795	2.0	370	10	AW170669	xi85g05.x
C 723	2.0	337	10	AU031985	AU031985	796	2.0	370	11	BG378423	UI-R-CU0-
C 724	2.0	337	11	BG627186	CC-esf1cL	797	2.0	370	11	C96639	C96639
C 725	2.0	337	11	BF458322	UI-M-BZ1-	798	2.0	371	10	AI117892	uc39g03.r
C 726	2.0	338	11	BI288594	UI-R-DK0-	799	2.0	371	10	AI359680	qy33h01.x
C 727	2.0	338	11	BE993303	UI-M-BZ1-	800	2.0	371	10	AL368169	MTBA22F05
C 728	2.0	339	10	AA725247	ai16b09.s	801	2.0	371	10	AW456371	UI-M-BH3-
C 729	2.0	340	10	AW020544	dfl1c10.y	802	2.0	371	10	AW950359	EST362439
C 730	2.0	340	10	AW085718	xb43c08.x	803	2.0	371	11	BG626209	CC-esf1cL
C 731	2.0	340	11	W74730	zd56a07.s1	804	2.0	371	11	BG812173	daf66h05.
C 732	2.0	340	11	BF272776	GA_EB001	805	2.0	372	10	AA748404	oa56b12.s
C 733	2.0	341	10	AV695430	AV695430	806	2.0	372	10	AW792139	DO1026-R
C 734	2.0	341	10	AW529323	UI-R-ET1-	807	2.0	372	10	AW920139	tx88e05.x
C 735	2.0	341	11	BF272535	GA_EB001	808	2.0	373	10	AI690720	sm97f06.y
C 736	2.0	341	11	BF462684	UI-M-CG0p	809	2.0	373	10	BE057180	BG372191
C 737	2.0	342	10	AV742957	AV742957	810	2.0	373	11	BG372191	UI-R-CV0-
C 738	2.0	343	10	AW044671	ww74a06.x	811	2.0	373	11	H00246	yj22a11.r1
C 739	2.0	343	10	AW634283	bl18g06.w	812	2.0	374	11	BF408154	UI-R-BJ2-
C 740	2.0	344	10	BE116785	UI-R-B51-	813	2.0	374	11	BF465582	UI-M-CG0p
C 741	2.0	345	10	BE663032	105724.MA	814	2.0	375	10	AU161967	AU161967
C 742	2.0	346	10	AI254339	qu65b05.x	815	2.0	375	11	BF275144	GA_EB002

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C 817	23	2.0	376	11	BF917425	IL3-UT011	C 890	23	2.0	404	10	AA216952	mt71e10.r
C 818	23	2.0	377	10	AI201315	qf71c04.x	C 891	23	2.0	404	10	AA216952	cr52g12.x
C 819	23	2.0	377	10	AW584377	NTF-HSP-2	C 892	23	2.0	404	10	AA216952	cr52g12.x
C 820	23	2.0	378	13	AO021775	CTF-HSP-2	C 893	23	2.0	405	10	AI511149	UI-R-BT0-
C 821	23	2.0	379	11	BG455899	FT070807P	C 894	23	2.0	405	10	AW311156	sg40q10.y
C 822	23	2.0	380	10	AW620714	s108f10.y	C 895	23	2.0	405	11	BI297551	UI-R-CV2-
C 823	23	2.0	380	10	BE760497	aq-1773.A	C 896	23	2.0	405	11	H73455	y48009.s1
C 824	23	2.0	381	10	AI395320	MA002908.	C 897	23	2.0	406	10	AI146145	UI-R-BT0-
C 825	23	2.0	381	10	AO101953	AO101953	C 898	23	2.0	406	10	AO078613	AO078613
C 826	23	2.0	381	11	BI293258	UI-R-DK0-	C 899	23	2.0	406	10	AW562937	660070A01
C 827	23	2.0	382	10	AI273536	q155b08.x	C 900	23	2.0	406	11	BG620675	602619561
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C 830	23	2.0	382	11	BI298957	UI-R-CV2-	C 903	23	2.0	406	11	N92556	z290h02.s1
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C 835	23	2.0	384	10	AA219152	zq16a08.r	C 908	23	2.0	408	11	BI400439	MI-P-AV1-
C 836	23	2.0	384	11	BF408655	UI-R-BJ2-	C 909	23	2.0	409	10	AI754325	cr23d12.x
C 837	23	2.0	385	11	AA156119	z045g08.s	C 910	23	2.0	409	10	AI858700	DLA05A06
C 838	23	2.0	385	11	BG627096	CC-esf1cL	C 911	23	2.0	409	11	BG662898	W141d02.x
C 839	23	2.0	386	10	AO029390	AO029390	C 912	23	2.0	409	11	BI288366	UI-R-DK0-
C 840	23	2.0	386	10	AW516950	q005a01.x	C 913	23	2.0	409	11	AI753436	cr10e08.x
C 841	23	2.0	386	13	AO456668	ndxb0050P	C 914	23	2.0	410	11	BF392953	UI-R-CA0-
C 842	23	2.0	388	10	AW457668	UI-W-BH3-	C 915	23	2.0	411	10	AI763551	UI-R-Y0-a
C 843	23	2.0	389	11	BF719595	ma042a09.	C 916	23	2.0	411	10	AV709751	AV709751
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C 845	23	2.0	390	13	AI2819579	2M009114	C 918	23	2.0	412	10	AW159738	z06d04.x
C 846	23	2.0	391	10	AI024618	ov52f11.x	C 919	23	2.0	412	10	BG374749	UI-R-CV1-
C 847	23	2.0	391	10	AI077575	0233h08.x	C 920	23	2.0	412	11	BG378496	UI-R-CU0-
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C 850	23	2.0	392	10	AA979748	MEST1-C12	C 923	23	2.0	414	11	AA425118	zV47C09.r
C 851	23	2.0	392	11	BI298590	UI-R-CV2-	C 924	23	2.0	414	11	BG373833	MI-P-AV1-
C 852	23	2.0	392	13	B78988	CTT-HSP-556	C 925	23	2.0	414	11	BF712341	MI-P-AV1-
C 853	23	2.0	393	10	AI128207	q047g09.x	C 926	23	2.0	414	11	BG194478	RSN13637
C 854	23	2.0	393	10	AI593392	UI-M-BZ1-	C 927	23	2.0	415	10	AI425021	t950d01.x
C 855	23	2.0	393	11	BI404284	MI-P-CF1-	C 928	23	2.0	415	10	AI799603	wg02c07.x
C 856	23	2.0	394	10	AA924121	UI-R-A1-d	C 929	23	2.0	415	10	RI3138	yf72e10.r1
C 857	23	2.0	394	10	AI274209	q146d02.x	C 930	23	2.0	416	10	AL501629	AL501629
C 858	23	2.0	394	10	AA601367	no16c05.s	C 931	23	2.0	416	10	AV758046	UI-R-CA0-
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C 860	23	2.0	395	10	AA911813	OK74f10.s	C 933	23	2.0	416	11	BG079525	H3041D12-
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C 863	23	2.0	396	11	BE996131	UI-M-BZ1-	C 936	23	2.0	418	10	AA835741	od66g04.s
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C 866	23	2.0	398	10	AI016996	ou92a08.x	C 939	23	2.0	418	11	T92195	ye17f09.s1
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C 868	23	2.0	398	10	AA265303	mu66g04.r	C 941	23	2.0	419	10	AA859622	UI-R-E0-b
C 869	23	2.0	398	10	BE669477	7e13d02.x	C 942	23	2.0	419	10	AW152559	xf76c11.x
C 870	23	2.0	398	11	BF465302	UI-M-CG0P	C 943	23	2.0	419	10	AW664138	hi04g12.x
C 871	23	2.0	398	11	BG272299	nab87a07	C 944	23	2.0	419	11	BG670871	DRNEHC09
C 872	23	2.0	400	10	AI335623	qt24e01.x	C 945	23	2.0	419	11	BI297368	UI-R-CV2-
C 873	23	2.0	400	10	AL373268	MTBA56G09	C 946	23	2.0	419	11	C97095	C97095 Rice
C 874	23	2.0	400	10	AW152441	xg64f06.x	C 947	23	2.0	420	10	AI571916	tr71b10.x
C 875	23	2.0	401	10	AL379076	MCBB42D08	C 948	23	2.0	420	10	AW588046	kp12d10.y
C 876	23	2.0	401	10	AA175746	ms94d05.r	C 949	23	2.0	420	10	BE054140	GA_Ea000
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C 878	23	2.0	401	11	R36866	yf52e04.s1	C 951	23	2.0	421	10	AA642437	ns30a05.s
C 879	23	2.0	401	11	BE994286	UI-M-CG0P	C 952	23	2.0	421	10	AL512003	AL512003
C 880	23	2.0	401	11	BG042207	su93b01.y	C 953	23	2.0	421	11	BI059437	IL3-UT011
C 881	23	2.0	402	10	AO037708	zk37d07.s	C 954	23	2.0	422	10	AW599486	qa87a02.y
C 882	23	2.0	402	10	AI753714	cr14b07.x	C 955	23	2.0	422	11	BG155431	sab4a11.
C 883	23	2.0	403	10	AI126202	q086f05.x	C 956	23	2.0	423	11	BI403015	MI-P-CF1-
C 884	23	2.0	403	10	AI339816	qk68f10.x	C 957	23	2.0	424	11	BG633062	GH19443.5
C 885	23	2.0	403	10	AI983521	wz33b10.x	C 958	23	2.0	424	11	BI298212	UI-R-CV2-
C 886	23	2.0	403	10	AW151977	xf71b11.x	C 959	23	2.0	425	10	AI376844	MTBB26G01
C 887	23	2.0	403	10	AW491800	UI-M-BH3-	C 960	23	2.0	425	10	BE638807	946014C08
C 888	23	2.0	403	11	BG631320	CC-esf1cL	C 961	23	2.0	425	11	BI298733	UI-R-CV2-

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ALIGNMENTS

RESULT 1
 BE603222 528 bp mRNA EST 02-MAR-2001
 LOCUS HVSMEH0102J16f Hordeum vulgare 5-45 DAP spike EST library
 DEFINITION HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0102J16f, mRNA sequence.
 ACCESSION BE603222 GI:13191083
 VERSION BE603222
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 528)
 AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Sasaki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
 TITLE Development of a genetically and physically anchored EST resource for barley genomics
 JOURNAL Unpublished (2000)
 COMMENT On Aug 21, 2000 this sequence version replaced gi:9860783.
 CONTACT: Wing RA
 CLEMSON UNIVERSITY
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293

Email: rwing@clemonson.edu
 Seq primer: ATTAACCTCCTCAATAAGG
 High quality sequence stop: 512.
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 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
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 HVCNDA0009 (5 to 45 DAP)"
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 /lab_host="SOLR"
 /note="Vector: lambdaDAP; Site_1: EcoRI; Site_2: XhoI; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders"
 BASE COUNT 97 a 181 c 182 g 68 t
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.3e-11;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 238 cgcacgcaagatctcggacgaccccaagagagacgacgagtcgaggtcgcgagtaca 297
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 Db 195 CGCACGCCAGATCTCGACGACGCCCAAGGAGGAGATCCAGGATCGGTGCGGAGTACA 254
 QY 298 tcagcttcacacggggagggccaa 322
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 Db 255 TCAGCTTCATCAGCGGGGAGGCCAA 279
 RESULT 2
 AU088581 AU088581 695 bp mRNA EST 31-MAR-2000
 LOCUS AU088581 Rice callus Oryza sativa cDNA clone C52742, mRNA sequence.
 DEFINITION AU088581
 ACCESSION AU088581
 VERSION AU088581.1 GI:7378310
 KEYWORDS EST.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 695)
 AUTHORS Sasaki, T. and Yamamoto, K.
 TITLE Rice cDNA from callus (2000)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@nri.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/PROJECT="RGP".
 C52742_12A.
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 /note="Vector: pBluescript II SK+; Site_1: Salt; Site_2: NotI; cDNA prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the Sali-NotI site of pBluescript II SK+ phagemid."
 BASE COUNT 124 a 245 c 232 g 88 t
 ORIGIN


```

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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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      /cultivar="Nipponbare"
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 tgggcatgagcgcctcgcttcgactacgt 409
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Db 128 TGGGCCATGAGCGCGCTCGCTTCGAGCTACGT 162

RESULT 6
LOCUS C19737 328 bp mRNA EST 24-OCT-1996
DEFINITION C19737 Rice panicle at ripening stage Oryza sativa cDNA clone
      Ei0861_1A, mRNA sequence.
ACCESSION C19737
VERSION C19737.1 GI:1632008
KEYWORDS EST.
SOURCE Oryza sativa.
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  AUTHORS Sasaki,T.
  TITLE Rice cDNA from panicle at ripening stage
  JOURNAL Unpublished (1996)
  COMMENT Contact: Takuji Sasaki
    National Institute of Agrobiological Resources
    Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
    305-8602, Japan
    Tel: 81-298-38-7441
    Fax: 81-298-38-7468
    Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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      /note="Organ: panicle; Rice cDNA from panicle at ripening
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 189 ctgatccgatcgcaacgtgatccgcacatcgcg 223
      |||||
Db 101 CTGATCCGATCGGACGATCGATCGCATCGCG 135

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Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 101 CTGATCCGATCGGACGATCGATCGCATCGCG 135

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RESULT 7
LOCUS AW670176 368 bp mRNA EST 25-APR-2001
DEFINITION 114040 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW670176
VERSION AW670176.1 GI:7526690
KEYWORDS EST.
SOURCE COW.
  ORGANISM
    Bos taurus
    Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
REFERENCE
  AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
    Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
    ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
    Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
    Keele,J.W.
  TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
    libraries and construction of a gene index for cattle
  JOURNAL Genome Res. 11 (4), 626-630 (2001)
  MEDLINE 21180013
  COMMENT Contact: Smith TPL
    USDA, ARS, US Meat Animal Research Center
    PO Box 166, Clay Center, NE 68933-0166, USA
    Tel: 402 762 4366
    Fax: 402 762 4390
    Email: smith@mail.marc.usda.gov
    Single pass sequencing. Bases called and alt_trimmed with phred
    v0.980904.e. Vector identified by cross_match with the -minscore 18
    and -minmatch 12 options.
    PCR Primers
    FORWARD: AGGAACAGCTATGACCAT
    BACKWARD: GTTTCCTCCAGTCACGACG
    Plate: 111 row: M column: 16
    Seq primer: ATTAGGTGACACTATAG.
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      /note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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ORIGIN

Query Match 2.3%; Score 27; DB 10; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1147 gattatttcaaaaaaaaaaaaaaaaaa 1173
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Db 249 GATTTATTTCAAAAAAAAAAAAAAAAAA 275

RESULT 8
LOCUS BF042068 387 bp mRNA EST 10-OCT-2000
DEFINITION BP250013A20D7 Soares normalized bovine placenta Bos taurus cDNA
      clone BP250013A20D7 5', mRNA sequence.
ACCESSION BF042068
VERSION BF042068.1 GI:10759195
KEYWORDS EST.
SOURCE COW.
  ORGANISM
    Bos taurus
    Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
    Bovinae; Bos.
REFERENCE
  1 (bases 1 to 387)

```

AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,
J.H.

TITLE Bovine ESTs

JOURNAL Unpublished (2000)

COMMENT Contact: Levin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length. REPEAT
IN THE SEQUENCE Simple_repeat STRAND (+) ELEMENT (A)n LOCATION [365
,386].

PCR PRIMERS
FORWARD: TAATAGCACTCCTACTATAGG
BACKWARD: ATTAACCTCCTAAAG
Insert Length: 387 Std Error: 0.00
Plate: BP250013A20 row: D column: 7
Seq primer: AGCGATAACAATTCCACACGGA
High quality sequence stop: 387.

FEATURES
SOURCE Location/Qualifiers
1..387
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250013A20D7"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pMT73pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT	149 a	66 c	65 g	107 t
ORIGIN				

Query Match	2.3%	Score 27;	DB 11;	Length 387;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;		
Matches	27;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy 1147 gattatttcacaaagaaaaaagaaaaa 1173
|||||
Db 356 GATTATTTCAAAAAAGAAAAAAGAAA 382
|||||

RESULT	9
AV385922	
LOCUS	AV385922 644 bp mRNA
DEFINITION	cDNA clone 007G18_3 3', mRNA sequence.
ACCESSION	AV385922
VERSION	AV385922.1 GI:6130979
KEYWORDS	EST.
SOURCE	Halocynthia roretzi.
ORGANISM	Halocynthia roretzi. Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Stolidobranchia; Pyuridae; Halocynthia. 1 (bases 1 to 644) Makabe,K.W. Halocynthia roretzi EST Unpublished (1999) Contact: Kazuhiro W. Makabe Department of Zoology, Graduate School of Science Kyoto University Sakyo-Ku, Kyoto, Japan

```

Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: kwmakabe@ascidian.zool.kyoto-u.ac.jp.

FEATURES
    source
        1. .644
        /organism="Halocynthia roretzi"
        /db_xref="taxon:7729"
        /clone="007G18_3"
        /clone_lib="Halocynthia roretzi Fertilized egg"
        /dev_stage="Fertilized egg"
        187 a 112 c 110 g 231 t 4 others
BASE COUNT
ORIGIN

Query Match 2.3%; Score 27; DB 10; Length 644;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1147 gattatttcaaaaaaaaaaaaaa 1173
|||||
DB 613 GATTATTTCAAAAA 639

RESULT 10
BF013366
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BF013366 67 bp mRNA EST 10-MAY-2001
rK26g04.y1 Meloidogyne javanica Egg SL1 Topo2 Kloeck Chiapelli
McCartester Meloidogyne javanica cDNA 5', mRNA sequence.
BF013366
BF013366.1 GI:10713690
EST.
root-knot nematode.
Meloidogyne javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchima;
Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 67)
McCartester,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,R.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCartester JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Andrew Kloeck
(kloeck@biology.wustl.edu) at Divergence LLC, and Brandi Chiapelli
(bchiapell@watson.wustl.edu) and Dr. Jim McCartester
(jmccartester@watson.wustl.edu) at Washington University Genome
Sequencing Center. DNA Sequencing by: Washington University Genome
Sequencing Center St. Louis.
Seq primer: SL1 primer.
Location/Qualifiers
1. .67
/organism="Meloidogyne javanica"
/db_xref="taxon:6303"
/clone_lib="Meloidogyne javanica Egg SL1 Topo2 Kloeck
Chiapelli McCartester"
/dev_stage="enriched for eggs"
/lab_host="DH10B"
/note="vector: pCRII-TOPO; SL1-Oligo(dT) PCR-based
library. Meloidogyne javanica cDNA PCR products of size
>400 nucleotides containing SL1 on the 5' end and oligo(dT)
on the 3' end were non-directionally cloned into
pCRII-TOPO (Invitrogen) following the Topo TA cloning
protocol. The cDNA insert can be excised by digestion with

```

```

Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: kwmakabe@ascidian.zool.kyoto-u.ac.jp.

FEATURES             source
    1. .644
        /organism="Halocynthia roretzi"
        /db_xref="taxon:7729"
        /clone="007G18_3"
        /clone_lib="Halocynthia roretzi Fertilized egg"
        /dev_stage="Fertilized egg"
BASE COUNT          187 a   112 c   110 g   231 t       4 others
ORIGIN

Query Match              2.3%; Score 27; DB 10; Length 644;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1147 gattatttcaaaaaaaaaaaaaaa 1173
|||||
DB 613 GATTATTTCAAAAAAAAAAAAAAA 639

RESULT 10
BF013366
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BF013366      67 bp      mRNA      EST      10-MAY-2001
rK26g04.y1 Meloidogyne javanica Egg SL1 Topo2 Kloeck Chiapelli
McCartier Meloidogyne javanica cDNA 5', mRNA sequence.
BF013366
BF013366.1 GI:10713690
EST.
root-knot nematode.
Meloidogyne javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 67)
McCartier,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,R.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCartier JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Andrew Kloeck
(kloeck@biology.wustl.edu) at Divergence LLC, and Brandi Chiapelli
(bchiapell@watson.wustl.edu) and Dr. Jim McCartier
(jmccartier@watson.wustl.edu) at Washington University Genome
Sequencing Center. DNA Sequencing by: Washington University Genome
Sequencing Center St. Louis.
Seq primer: SL1 primer.
Location/Qualifiers
    1. .67
        /organism="Meloidogyne javanica"
        /db_xref="taxon:6303"
        /clone_lib="Meloidogyne javanica Egg SL1 Topo2 Kloeck
Chiapelli McCartier"
        /dev_stage="enriched for eggs"
        /lab_host="DH10B"
        /note="vector: pCRII-TOPO; SL1-Oligo(dT) PCR-based
library. Meloidogyne javanica cDNA PCR products of size
>400 nucleotides containing SL1 on the 5' end and oligo(dT)
on the 3' end were non-directionally cloned into
pCRII-TOPO (Invitrogen) following the ToPo TA cloning
protocol. The cDNA insert can be excised by digestion with

```

ECORI. The library was constructed by Dr. Andrew Kloek at Divergence LLC and Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. Nematodes were provided by Dr. David Bird of North Carolina State University."

BASE COUNT 26 a 17 c 3 g 21 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.8e+03; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||

DB 10 ATTATTTCAAAAAA 35

RESULT 11
BI268661 152 bp mRNA EST 18-JUL-2001
LOCUS NF015H10GS1F1091 Germinating Seed Medicago truncatula cDNA clone
DEFINITION NF015H10GS 5', mRNA sequence.
ACCESSION BI268661
VERSION BI268661.1 GI:14874736
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 152)
AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula germinating seed library
JOURNAL Unpublished (2001)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 152 Std Error: 0.00
Plate: 015 row: H column: 10
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
source
1..152
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF015H10GS"
/clone_lib="Germinating seed"
/tissue_type="germinating seeds"
/dev_stage="0, 1, 2 and 3 days after acid treatment."
/note="Vector: Lambda Zap; M. truncatula seeds were acid treated and placed on wet filter papers in petri dishes. Seeds were harvested at 0, 1, 2 and 3 days after acid treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each time point. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene).
Excised plasmids were plated using SOUR cells."

BASE COUNT 70 a 24 c 16 g 42 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 152;

Best Local Similarity 100.0%; Pred. No. 4.7e+03; Mismatches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||

DB 120 ATTATTTCAAAAAA 145

RESULT 12
BG379246 153 bp mRNA EST 12-MAR-2001
LOCUS UI-R-BT1-bnn-c-04-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
DEFINITION UI-R-BT1-bnn-c-04-0-UI 3', mRNA sequence.

ACCESSION BG379246
VERSION BG379246.1 GI:13303718
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 153)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-27,
>AT_rich_low_complexity
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1..153
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BT1-bnn-c-04-0-UI"
/clone_lib="UI-R-BT1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at rattus.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BT1
TAG_TISSUE=corpus-striatum
TAG_SEQ=CFAGG"

BASE COUNT 32 a 29 c 37 g 55 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 153;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaaaaaa 1173
|||||
Db 26 ATTATTTCACAAAAA

RESULT 13

AW356324 177 bp mRNA EST 25-APR-2001
LOCUS 38607 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION AW356324
ACCESSION AW356324
VERSION AW356324.1 GI:5860330
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 177)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGACG

Plate: 19 row: F column: 14

Seq primer: ATTATGCTGACACTATAG.

Location/Qualifiers

1..177

/Organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2BOV"

/tissue_type="pooled"

/lab_host="DH108"

/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from testis, thymus,

semitendinosus muscle, longissimus muscle, pancreas,

adrenal, and endometrium."

62 a 22 c 17 g 76 t

BASE COUNT

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaaaaaa 1173
|||||

Db 151 ATTATTTCACAAAAA

RESULT 14

BG735393 304 bp mRNA EST 15-MAY-2001
LOCUS cc-escf1ELF707d1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA, mRNA sequence.

ACCESSION BG735393
VERSION BG735393.1 GI:14085082
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE 1 (bases 1 to 304)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutgers S. van der Hoeven

Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
3 prime sequence.

FEATURES
source
1..304

/Organism="Lycopersicon esculentum"

/cultivar="56203"

/db_xref="taxon:4081"

/clone_lib="tomato flower library from a mixture of

developmental stages"

/tissue_type="developing flower buds and open flowers"

/dev_stage="4-8 week old plants"

/lab_host="XL0LR"

/note="vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;

Flowers and flower buds were collected from greenhouse

grown plants and used for library construction (cLEL)."

122 a 48 c 40 g 94 t

BASE COUNT

ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaa 1173
|||||

Db 26 ATTATTTCACAAAAA

RESULT 15

BG735487/c 341 bp mRNA EST 15-MAY-2001
LOCUS cc-escf1EL8J20d1 Tomato flower library from a mixture of
DEFINITION developmental stages Lycopersicon esculentum cDNA, mRNA sequence.

ACCESSION BG735487
VERSION BG735487.1 GI:14085176
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE 1 (bases 1 to 341)
AUTHORS van der Hoeven,R.S. and Tanksley,S.D.
TITLE ESTs from a tomato flower library
JOURNAL Unpublished (2001)
COMMENT Contact: Rutgers S. van der Hoeven

Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
3 prime sequence.

FEATURES
source
1..341

```

/organism="Lycopersicon esculentum"
/cultivar="F6203"
/db_xref="taxon:4081"
/clone_lib="tomato flower library from a mixture of
developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XLOLR"
/notes="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cLEL)."
BASE COUNT      98 a      58 c      56 g      129 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 26 ATTATTTCACAAAAAAAAAAAAAAAAA 1

RESULT 16
Bg603362
LOCUS
DEFINITION
EST502452 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
clone PYCDQ79, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Plasmodium yoelii.
Plasmodium yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE
1 (bases 1 to 342)
Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,
Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,
Hoffman,S.L. and Nussenzweig,V.
Exploring the transcriptome of the malaria sporozoite stage
Proc. Natl. Acad. Sci. U. S. A. 98 (17), 9895-9900 (2001)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Request for clones, please contact: Stefan Kappe,
kappes01@opmail.med.nyu.edu Michael Heidelberg Division,
Department of Pathology New York University School of Medicine.
FEATURES
source
Location/Qualifiers
1..342
/organism="Plasmodium yoelii"
/strain="17XNL"
/db_xref="taxon:5861"
/clone="PYCDQ79"
/clone_lib="Plasmodium yoelii sporozoite cDNA"
/dev_stage="sporozoites from salivary gland"
/lab_host="E. coli TOP10"
/notes="Vector: pCR4; TA cloning; Plasmodium yoelii
sporozoite cDNA library from salivary gland sporozoites 14
days post-infection"
BASE COUNT      180 a      30 c      27 g      105 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 342;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||

```

```

Db 265 ATTATTTCACAAAAAAAAAAAAAAAAA 290

RESULT 17
Bg603362
LOCUS
DEFINITION
EST50247/c
t175a01.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2137800 3',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 359)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco.
FEATURES
source
Location/Qualifiers
1..359
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2137800"
/clone_lib="NCI-CGAP_Kid11"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT      125 a      68 c      39 g      127 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 31 ATTATTTCACAAAAAAAAAAAAAAAAA 6

RESULT 18
Bg625968/c
LOCUS
DEFINITION
EST5025968/c
BG625968
cc-esflicLEL10F17a1 Tomato flower library from a mixture of
developmental stages Lycopersicon esculentum cDNA clone
cc-esflicLEL10F17a1, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

```


Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopodiaceae.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 361)
van der Hoeven,R.S. and Tanksley,S.D.
ESTs from a tomato flower library
Unpublished (2001)
Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu

3 prime sequence.
Location/Qualifiers
1..361
/organism="Lycopodium esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="CC-esfLcLE110F17a1"
/clone_lib="tomato flower library from a mixture of developmental stages"
/tissue_type="developing flower buds and open flowers"
/dev_stage="4-8 week old plants"
/lab_host="XLOLR"
/lab_host="XLOLR"
/note="vector: PBK,CMV; Site_1: EcoRI; Site_2: XhoI; Flowers and flower buds were collected from greenhouse grown plants and used for library construction (cLEL)."
BASE COUNT 131 a 73 c 61 g 95 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
||||| 1173
Db 26 ATTATTTCAAAAA 1

RESULT 19
BF419934/c 379 bp mRNA EST 28-NOV-2000
LOCUS
DEFINITION
UI-R-BJ2-bph-h-10-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bph-h-10-0-UI 3', mRNA sequence.
ACCESSION
BF419934
VERSION
BF419934.1 GI:11407923
KEYWORDS
EST.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

1 (bases 1 to 379)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
9704477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA Library Preparation: M.B. Soares Lab

Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers

1..379
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bph-h-10-0-UI"
/clone_lib="UI-R-BJ2"
/lab_host="DHI0B (Life Technologies)"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB="UI-R-BJ2"
TAG_TISSUE="heart"
TAG_SEQ="ACAAAC"

BASE COUNT 87 a 89 c 104 g 99 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
||||| 1173
Db 26 ATTATTTCAAAAA 1

RESULT 20
BG652352/c

LOCUS
DEFINITION
BG652352 384 bp mRNA EST 25-APR-2001
sad65h07.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl051-5342 5', mRNA sequence.

ACCESSION
BG652352
VERSION
BG652352.1 GI:13789761
KEYWORDS
EST.
SOURCE
soybean.

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 384)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

TITLE

JOURNAL

COMMENT

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info.genomesystems.com web site: www.genomesystems.com

```

Putative full length read
vector to vector length is 385.
FEATURES
  source
    1..384
      /organism="Glycine max"
      /db_xref="taxon:3847"
      /clone="GENOME SYSTEMS CLONE ID: Gm-cl051-5342"
      /clone_lib="Gm-cl051"
      /tissue_type="floral meristematic mRNA"
      /lab_host="DH10B"
      /note="Vector: pluescript II SK+; Site_1: EcoRI; Site_2:
      XhoI; The cDNA library was constructed from floral
      meristematic mRNA provided by Dr. Halina Knap of Clemson
      University. Complementary DNA was synthesized from mRNA
      using a primer consisting of a poly(dT) sequence with a
      XhoI restriction site. EcoRI adapters were ligated to the
      blunt-ended cDNA fragments followed by XhoI digestion. The
      cDNA fragments were directionally cloned into the
      EcoRI-XhoI restriction site of the pBluescript vector. The
      ligated cDNA fragments were transformed into DH10B host
      cells (GibcoBRL). This library was constructed in the
      laboratory of Dr. Randy Shoemaker."
BASE COUNT      111 a      89 c      37 g      147 t
ORIGIN

Query Match      2.2%; Score 26; DB 11; Length 384;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 31 ATTATTTCACAAAAA
|||||

RESULT 21
AW692142/c
LOCUS
DEFINITION
  NF052F06STF1000 Developing stem Medicago truncatula cDNA clone
  NF052F06ST 5', mRNA sequence.
ACCESSION
  AW692142
VERSION
  AW692142.2 GI:11957103
KEYWORDS
  EST.
SOURCE
  Medicago truncatula
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
  Medicago.
REFERENCE
  1 (bases 1 to 458)
  He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
  ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
  ,R.A.
  Expressed Sequence Tags from the Samuel Roberts Noble Foundation
  Medicago truncatula stem library
  Unpublished (2000)
  On Apr 14, 2000 this sequence version replaced gi:7566878.
  Contact: Dixon RA
  Plant Biology Division
  The Samuel Roberts Noble Foundation
  2510 Sam Noble Parkway, Ardmore, OK 73402, USA
  Tel: 580 221 7302
  Fax: 580 221 7380
  Email: radixon@noble.org
  Insert Length: 692 Std Error: 0.00
  Plate: 052 row: F column: 06
  Seq primer: TCACACAGGAAACGCTATGAC.
FEATURES
  source
    1..458
      /organism="Medicago truncatula"
      /db_xref="taxon:3880"
      /clone="NF052F06ST"
      /clone_lib="Developing stem"

```

```

/tissue_type="stem"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
BASE COUNT      146 a      82 c      77 g      153 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 52 ATTATTTCACAAAAA
|||||

RESULT 22
AW790703
LOCUS
DEFINITION
  D00136-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
  cDNA clone D00136 similar to nadh-ubiquinone oxidoreductase 9.5 kd
  subun, mRNA sequence.
ACCESSION
  AW790703
VERSION
  AW790703.1 GI:13902300
KEYWORDS
  EST.
SOURCE
  Blumeria graminis f. sp. hordei.
  Blumeria graminis f. sp. hordei
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
  Erysiphales; Erysiphaceae; Blumeria.
REFERENCE
  1 (bases 1 to 458)
  Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver
  ,R.P.
  Gene identification in the fungal pathogen Blumeria graminis by
  expressed sequence tag analysis
  Unpublished (2000)
  Contact: Rasmussen,S.W.
  Department of Yeast Genetics
  Carlsberg Laboratory
  10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
  Tel: 45 3327 5230
  Fax: 45 3327 4766
  Email: sw@erc.dk
  High quality sequence stop: 458
  POLYA=Yes.
FEATURES
  source
    1..458
      /organism="Blumeria graminis f. sp. hordei"
      /db_xref="taxon:62688"
      /clone="D00136"
      /clone_lib="Lambda Zap, Stratagene"
      /cell_type="conidia"
      /lab_host="Hordeum vulgare"
BASE COUNT      153 a      94 c      86 g      125 t
ORIGIN

Query Match      2.2%; Score 26; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 432 ATTATTTCACAAAAA
|||||

RESULT 23
AW790704
LOCUS
DEFINITION
  D00136-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei
  cDNA clone D00136 similar to nadh-ubiquinone oxidoreductase 9.5 kd
  subun, mRNA sequence.
ACCESSION
  AW790704

```

```

VERSION      AW790704.1  GI:13902301
KEYWORDS
SOURCE       Blumeria graminis f. sp. hordei.
ORGANISM     Blumeria graminis f. sp. hordei
REFERENCE    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
AUTHORS      Erysiphales; Erysiphaceae; Blumeria.
             Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Roustier,J.A. and Oliver
             ,R.P.
TITLE        Gene identification in the fungal pathogen Blumeria graminis by
JOURNAL      expressed sequence tag analysis
COMMENT      Unpublished (2000)
             Contact: Rasmussen,S.W.
             Department of Yeast Genetics
             Carlsberg Laboratory
             10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
             Tel: 45 3327 5230
             Fax: 45 3327 4766
             Email: swr@crc.dk
             High quality sequence stop: 458
             POLYA=yes.

FEATURES
  source
    Location/Qualifiers
      1..458
        /organism="Blumeria graminis f. sp. hordei"
        /db_xref="taxon:62688"
        /clone="D00136"
        /clone_lib="Lambda Zap, Stratagene"
        /cell_type="conidia"
        /lab_host="Hordeum vulgare"
        /lab_host="94 c 86 g 125 t"

BASE COUNT  153 a 153 a 86 g 125 t
ORIGIN
Query Match      2.2%; Score 26; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaaaaaa 1173
Db 432 ATTATTTCACAAAAAATAAAAAA 457

RESULT 24
LOCUS      B1312519/c
DEFINITION daf92h05.x1 NICHG XGC Eye1 Xenopus laevis cDNA clone IMAGE:4757624
3', mRNA sequence.
ACCESSION  B1312519
VERSION    B1312519.1  GI:14986846
KEYWORDS   EST.
SOURCE     African clawed frog.
ORGANISM   Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
REFERENCE  1 (bases 1 to 484)
AUTHORS    Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
            Martin,J., Wyllie,T., Underwood,K., Theising,B., Bowers,Y., Person
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
            Waterston,R. and Wilson,R.
            WashU Xenopus EST project, 1999
            Unpublished (1999)
            Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 275.

FEATURES
  source
    Location/Qualifiers
      1..464
        /organism="Xenopus laevis"
        /db_xref="taxon:8355"
        /clone="IMAGE:4757624"
        /clone_lib="NICHG XGC Eye1"
        /dev_stage="adult"
        /lab_host="DH10B (phage-resistant)"
        /notes="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
            Average insert size 2.3 kb. Constructed by Life
            Technologies. Note: This is a Xenopus Gene Collection (XGC
            ) library."

BASE COUNT  173 a 173 a 80 c 60 g 151 t
ORIGIN
Query Match      2.2%; Score 26; DB 11; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaaaaaaaaaaaaaa 1173
Db 29 ATTATTTCACAAAAAATAAAAAA 4

RESULT 25
LOCUS      AL385635
DEFINITION MCBC29F10r1 MtBC Medicago truncatula cDNA clone MtBC29F10 T7, mRNA
sequence.
ACCESSION  AL385635
VERSION    AL385635.1  GI:9685386
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE  1 (bases 1 to 469)
AUTHORS    Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
            Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
            ,V. and Gamas,P.
            Medicago truncatula ESTs from endomycorrhizal roots
            Unpublished (2000)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
            Biologie Moleculaire des Relations Plantes-Microorganismes,
            CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
            Mt-est@toulouse.inra.fr Website :
            http://sequence.toulouse.inra.fr/Mtruncatula.html).
            Location/Qualifiers
              1..469
                /organism="Medicago truncatula"
                /cultivar="Jemalong"
                /db_xref="taxon:3880"
                /clone="MtBC29F10"
                /clone_lib="MtBC"
                /tissue_type="arbuscular mycorrhiza"
                /dev_stage="harvested 3 weeks post inoculation with Glomus
                intraradices"
                /note="vector: pBluescript pSK; Site_1: EcoRI; Site_2:
                XhoI; M. truncatula sterilised seeds were germinated for
                72h at 25 C, before transplanting into a 1/3 Epsilones soil
                : 2/3 calcined terragreen mix in the presence of onion
                root fragments colonized by the arbuscular mycorrhizal

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embryonic stages). Each library was normalized individually according to the procedure described by Bonaldo, Lennon & Soares (Genome Research 6: 791-806, 1996). For construction of the DKO subtracted library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), aorta (CWOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG_LIB-UI-R-DKO
TAG_TISSUE-rat placenta pool
TAG_SEQ-TCACGACGT

BASE COUNT 151 a 92 c 73 g 159 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 26 ATTATTTCAAAAAAAAAAAAAA 1

RESULT 28

AI302809/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Human

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 373 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 450.

FEATURES

Location/Qualifiers

1..488

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1902486"

/clone_lib="NCI_CGAP_Kid5"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/notes="Organ: kidney; Vector: pT73b-Pac (Pharmacia) with

a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGGAAGAATTCGGCGCGCAATATTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

"

BASE COUNT 147 a 85 c 88 g 168 t

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 488;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attattcaaaaaa1173

Db 33 ATTATTTCAAAAAAAAAAAAAA 8

RESULT 29

AI588492/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Rasbora; Danio.

1 (bases 1 to 490)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy

, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood

, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,

Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,

Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.

and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrfish@wustl.edu

cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center. Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimatendatenbank, Berlin, Germany (web address:

www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:

gil25948581gb|AA658704|AA658704 fa56c02.sl zebrafish gridded kidney

Danio

Seq primer: T7 ET from Amersham

High quality sequence stop: 423

POLYA-No.

Location/Qualifiers

1..490

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="IMAGE:3720245"

/clone_lib="Zebrafish WashU MPIMG EST"

intraradices" /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 °C, before transplanting into a 1/3 Espisses soil : 2/3 calcined Terragreen mix in the presence of onlon root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack XL packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de séquençage (Genoscope, Evry, France). Note : EST may be of fungal origin."

a 51 c 46 g 222 t

```
Query Match      2.2%; Score 26; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e-03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT	31				
AI974955/c					
LOCUS	AI974955	513 bp	mrna	EST	27-AUG-1999
DEFINITION	EST269549	Schistosoma mansoni	female, Phil Loverde	Joe Merrick	
		Schistosoma mansoni	CDNA clone SMFAA16	5' end similar to actin,	
				mrna sequence.	
ACCESSION	AI974955				
VERSION	AI974955.1	GI:5788123			
KEYWORDS	EST				
SOURCE	Schistosoma mansoni.				
ORGANISM	Schistosoma mansoni.				
	Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;				
	Rhabdophora; Eutelethophora; Reversoepmacta; Mediofusata;				
	Neodermata; Trematoda; Digenea; Strigeida; Schistosomatoidae;				
	Schistosomatidae; Schistosoma.				
REFERENCE	1 (bases 1 to 513)				
AUTHORS	Merrick, J.M., Osman, A., Loverde, P.T., Chandra, I., Glodek, A., Fraser				
	.C.M. and Lee, N.H.				

REFERENCE AUTHORS	Schistosoma indicum, Schistosoma 1 (bases 1 to 513) Merrick,J.M., Osman,A., LoVerde,P.T., Chandra,I., Glodex,A., Fraser ,C.M. and Lee.N.H.
TITLE	Generation of a Schistosoma sp. EST (SWESt) Catalog & Schistosome Gene Index
JOURNAL COMMENT	Unpublished (1998) Contact: Norman H. Lee The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3529 Fax: 301 838 0208 Email: nhlee@tigr.org Seq primer: M13 Reverse.

```

FEATURES
    source
        Location/Qualifiers
            1. .513
                /organism="Schistosoma mansoni"
                /db_xref="taxon:6183"
                /clone="SMFAA16"
                /clone_lib="Schistosoma mansoni female, Phil Loverde/Joe
                Merrick"
                /sex="female"
                /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhoI
                ; directionally cloned cDNAs"
            151 a      110 c      88 g      164 t
BASE COUNT
ORIGIN

```

Query Match 2.2%; Score 26; DB 10; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaa 1173

|||||

Db 66 ATTATTTCAAAAAAAAAAAAAAAAA 41

RESULT 32
 AW066395/c 530 bp mRNA EST 30-MAR-2000
 LOCUS 687001H02.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
 DEFINITION
 ACCESSION AW066395
 VERSION AW066395.1 GI:6021467
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 JOURNAL clade; Panicoideae; Andropogoneae; Zea.

COMMENT
 1 (bases 1 to 530)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 687001 row: H column: 02.

FEATURES
 Location/Qualifiers

1..530
 /organism="Zea mays"
 /cultivar="Illinois High Oil"
 /db_xref="taxon:4577"
 /clone_lib="687 - Early embryo from Delaware"
 /tissue_type="embryo"
 /dev_stage="14, 21, 28, and 35 days after pollination"
 /lab_host="E. coli SOLR"
 /note="Organ: embryo; Vector: pBluescript SK; Site_1: xhoI
 ; Site_2: EcoRI; Library was prepared by Statagene using
 the Uni-ZAP XR system (Stratagene BN937328-12). Clones
 were picked by a Q-bot after blue/white selection
 (ampicillin resistance - use 100 micrograms/microliter).
 Developed from a pool of equal amounts of RNA from
 developing embryos sampled at 14, 21, 28 and 35 days after
 pollination of the Illinois High Oil Maize Strain Cycle
 90. This closed strain has been selected for high oil
 concentration for 90 generations and originates from the
 1890s era open pollinated variety Burr's White"

BASE COUNT 147 a 116 c 112 g 155 t

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 530;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaa 1173

|||||

Db 54 ATTATTTCAAAAAAAAAAAAAAAAA 29

RESULT 33
 AW700042/c 546 bp mRNA EST 18-APR-2000
 LOCUS gb37h12.y1 Moss EST library PPN Physcomitrella patens cDNA clone
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AW700042.1 GI:7584145

EST.

Physcomitrella patens.

Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 546)

Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C., Clifton
 S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood
 K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T.,
 Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.

Leeds/Wash U Moss EST Project

Unpublished (1999)

Contact: Ralph Quatrano

Leeds/Wash U Moss EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Libraries were constructed by Dr. Stavros Bashardes as part of the
 Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
 Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
 University Genome Sequencing Center For information on obtaining a
 clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 173.

FEATURES

source

1..546
 /organism="Physcomitrella patens"
 /db_xref="taxon:3218"
 /clone_lib="Moss EST library PPN"
 /tissue_type="protonemata: 7 day old tissue auxin treated"
 /lab_host="DH10B"
 /note="Vector: pBluescript SK; Site_1: EcoRI; Site_2:
 xhoI; Construction of the cDNA library was carried out
 using Stratagene's 'Unizap' - cDNA synthesis kit'. cDNA was
 constructed using an oligo dT primer/linker that contains
 a XhoI site within it. Following ds cDNA synthesis,
 EcoRI adapters were ligated to the blunt ends and sample
 was digested with XhoI. The result is cDNA with an EcoRI
 sticky end on one side and a XhoI sticky end on the other.
 This cDNA was ligated directionally in Unizap arms. The
 vector is designed containing the pBluescript sequence as
 well as lambda DNA and cDNA is cloned within this
 pBluescript sequence. The vector was then packaged using
 Gold gigaPackaging extracts. Library was grown in XlBlue
 MRF' cells and amplified. The library was excised by mass
 excision using Stratagene's 'Mass excision kit' that uses
 exsist as a helper phage that releases the pBluescript
 sequence and circularises it as single stranded plasmids
 that are then packaged (by helper phage) and secreted out
 of the host cell as phagemids. SOLR cells were transformed
 with phagemids and the library was plated out on LB-amp
 plates to select for transformants. Approximately 1,000
 ,000 colonies were grown and recovered. The double
 stranded plasmid library was recovered by using Qulagen
 Midi prep kit. 2 micro grams of each library were used to
 transform DH10B cells by electroporation."

BASE COUNT 153 a 143 c 100 g 150 t

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 546;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaa 1173

|||||
Db 39 ATTATTTCAAAAAAAAAAAAAAAAAAAAA 14

RESULT 34

AW067352/c

LOCUS

DEFINITION

mays cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 554)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 683022 row: G column: 01.

Location/Qualifiers

1. .554

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone_lib="683 - 14 day immature embryo from Hake lab (HS

)"

/tissue_type="embryo"

/dev_stage="14 days after pollination"

/lab_host="DH10B"

/note="Organ: embryo; Vector: pBKCMV (Stratagene's zap

Express); Site:1: XhoI; Site:2: EcoRI; Directionally

cloned, 14 day immature embryo library created with

Stratagene's Zap Express cDNA protocol."

BASE COUNT 153 a 151 c 122 g 128 t

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 554;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaaaaaa 1173

|||||

Db 29 ATTATTTCAAAAAAAAAAAAAAAAAAAAA 4

RESULT 35

AI450987/c

LOCUS

DEFINITION

mt12f02.x1 Soares mouse 3NDMS Mus musculus cDNA clone IMAGE:620859

3' similar to TR:Q13535 Q13535 FRAP-RELATED PROTEIN ;, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 584)

Marra, M., Hillier, L., Kucuba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

house mouse.

Mus musculus

EST.

AI450987.1 GI:4300843

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 584)

Marra, M., Hillier, L., Kucuba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

TITLE
JOURNAL
COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 228.

Location/Qualifiers

1. .584

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone_image="IMAGE:620859"

/clone_lib="Soares mouse 3NDMS"

/sex="male"

/tissue_type="Spleen"

/dev_stage="4 weeks"

/lab_host="DH10B"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified

polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified p7T3 vector. RNA

provided by Dr. Bertrand Jordan. Library went through

three rounds of normalization, and was constructed by

Bento Soares and M.Fatima Bonaldo."

BASE COUNT 155 a 132 c 103 g 194 t

ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 584;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaaaaaaaaaaaaaaaaaa 1173

|||||

Db 27 ATTATTTCAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 36

BF646151

LOCUS

DEFINITION

clone NF067A10EC1F1072 Elicited cell culture Medicago truncatula cDNA

clone NF067A10EC 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 618)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation -

Center for Medicago Genomics Research

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

BF646151.1 GI:11911281

EST.

barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 618)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation -

Center for Medicago Genomics Research

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380

Email: radixon@noble.org
Insert Length: 618 Std Error: 0.00
Plate: 067 row: A column: 10
Seq primer: TCACACGAGAAACAGCTATGAC.

FEATURES

Location/Qualifiers
1..618
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF067A10EC"
/clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

BASE COUNT 211 a 119 c 119 g 167 t 2 others
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
Db 585 ATTATTTCAAAAA 610

RESULT 37
AZ369897/c
LOCUS 623 bp DNA GSS 02-OCT-2000
DEFINITION 1M0120N12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0120N12 R, DNA sequence.

ACCESSION AZ369897
VERSION AZ369897.1 GI:10483597
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 623)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0120 row: N column: 12
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 623.

FEATURES
source
1..623
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0120N12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 182 a 104 c 119 g 217 t 1 others
ORIGIN

Query Match 2.2%; Score 26; DB 13; Length 623;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1148 attatttcaaaaaa 1173
|||||
Db 219 ATTATTTCAAAAA 194

RESULT 38
BF294174/c
LOCUS 641 bp mRNA EST 04-MAY-2001
DEFINITION 001PB02 Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali
Plasmodium berghei cDNA 5', mRNA sequence.

ACCESSION BF294174
VERSION BF294174.1 GI:13942740
KEYWORDS EST.
SOURCE Plasmodium berghei.

ORGANISM Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 641)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Department of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: T3.

FEATURES

Location/Qualifiers
1..641
/organism="Plasmodium berghei"
/strain="ANKA clone HP (gametocyte producer)"
/db_xref="taxon:5821"
/clone_lib="Pb cDNA #17, Tommaso Pace, Marta Ponzi, and Clara Frontali"
/dev_stage="asynchronous blood stage"
/lab_host="Wistar rats"
/note="Vector: pBluescript II vector DNA, excised from Lambda Zap II.; Site_1: ECORI; Site_2: XhoI; Total RNA was extracted from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei, grown in Wistar rats to 30% parasitemia and 2-5% gametocytemia. Contaminating host

white cells had previously been removed and final host cell contamination estimated to be approximately 5%. PolyA+ RNA was extracted and reverse transcribed using an oligo dt-xhoI primer (Lambda ZAP II cDNA cloning kit, Stratagene). Second strand cDNA was made following the manufacturer's protocol. EcoRI adaptors were ligated to the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

BASE COUNT 278 a 67 c 63 g 233 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 641;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 31 ATTATTTCAAAAAAAAAAAAAAAAAA 6

RESULT 39
BI094602 683 bp mRNA EST 20-JUN-2001
LOCUS LBSSH00034 Preinfection stage symbiosis-regulated cDNAs from L.
DEFINITION bicolor x P. resinosa Laccaria bicolor cDNA, mRNA sequence.
ACCESSION BI094602
VERSION BI094602.1 GI:14516079
KEYWORDS EST.
SOURCE Laccaria bicolor.

ORGANISM Laccaria bicolor
REFERENCE Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
AUTHORS Agaricales; Tricholomataceae; Laccaria.
TITLE 1 (bases 1 to 683)
JOURNAL Podila G.K., Brand J.R. and Hynes M.J.
COMMENT Preinfection stage symbiosis-regulated cDNAs from L. bicolor x P. resinosa

Unpublished (2001)
Contact: Dr. G.K. Podila
Department of Biological Sciences
Michigan Technological University
1400 Townsend Drive, Houghton, MI 49931, USA
Tel: 906 487 3068
Fax: 906 487 3167
Email: gkpodila@mtu.edu.
Location/Qualifiers
1..683
/organism="Laccaria bicolor"
/db_xref="taxon:29883"
/clone_lib="Preinfection stage symbiosis-regulated cDNAs from L. bicolor x P. resinosa"
/note="cDNA clones were selected using a combination of suppressive subtraction hybridization derived probes and a cDNA library of L. bicolor, prepared from pooled RNA of interaction time points ranging from 6-72 h. Differential expression of these cDNAs was confirmed through screening a membrane array of the cDNAs with exponential probes prepared from control RNA obtained from free living L. bicolor and pooled interaction RNA."

BASE COUNT 261 a 90 c 118 g 214 t
ORIGIN

Query Match 2.2%; Score 26; DB 11; Length 683;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 647 ATTATTTCAAAAAAAAAAAAAAAAAA 672

RESULT 40

AW331967/c
LOCUS

DEFINITION
SlC6 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
sequence.

ACCESSION
AW331967

VERSION
AW331967.1 GI:6828233

KEYWORDS
EST.

SOURCE
Pneumocystis carinii f. sp. carinii.
ORGANISM Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.

REFERENCE
1 (bases 1 to 718)

AUTHORS
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.

TITLE
Expressed sequence tags from Pneumocystis carinii

JOURNAL
Unpublished (2000)

COMMENT
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
1..718
/organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
/lab_host="E. coli"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

BASE COUNT 290 a 98 c 85 g 245 t
ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 718;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 26 ATTATTTCAAAAAAAAAAAAAAAAAA 1

RESULT 41
AW331951/c

LOCUS

DEFINITION
SlA11 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
sequence.

ACCESSION
AW331951

VERSION
AW331951.1 GI:6828217

KEYWORDS
EST.

SOURCE
Pneumocystis carinii f. sp. carinii.
ORGANISM Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.

REFERENCE
1 (bases 1 to 794)

AUTHORS
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.

TITLE
Expressed sequence tags from Pneumocystis carinii

JOURNAL
Unpublished (2000)

COMMENT
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717

FEATURES
source
Email: stabenepop.uky.edu.
Location/Qualifiers
1. .794
/organism="Pneumocystis carinii f. sp. carinii"
/db_xref="taxon:38081"
/clone_lib="AGS-1"
/lab_host="E. coli"
/note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dt priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/pneumocystis/"

BASE COUNT 278 a 135 c 113 g 268 t
ORIGIN

Query Match 2.2%; Score 26; DB 10; Length 794;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 27 ATTATTTCAAAAAAAAAAAAAAAAAA 2

RESULT 42
BG151615/c
LOCUS
DEFINITION naq62b09.x1 NCI_CGAP_Co26 Homo sapiens cDNA clone IMAGE:4225889 3',
mRNA sequence.
ACCESSION BG151615
VERSION BG151615.1 GI:12663645
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 100)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov

Seq primer: -400P from Gibco.

FEATURES
source

1. .100
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4225889"
/clone_lib="NCI_CGAP_Co26"
/tissue_type="normal colonic mucosa"
/lab_host="DH10B"
/note="Organ: colon; Vector: pAMP1; mRNA made from normal
colonic mucosa, cDNA made by oligo-dt priming.
Directionally cloned into UDG sites. Size-selected on
agarose gel, average insert size 300 bp. Primary library.
CDNA library preparation: David B. Krizman, Ph.D.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

BASE COUNT 25 a 22 c 13 g 40 t
ORIGIN

Query Match 2.1%; Score 25; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 54 TTATTTCAAAAAAAAAAAAAAAAAA 30

RESULT 43

AI348819 151 bp mRNA EST 16-FEB-1999
LOCUS ta90e02.x2 NCI_CGAP_Brn20 Homo sapiens cDNA clone IMAGE:2051354 3',
mRNA sequence.
DEFINITION

ACCESSION AI348819
VERSION AI348819.1 GI:4086025
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 151)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 235 Std Error: 0.00
Seq primer: -400P from Gibco.

FEATURES
source

1. .151
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2051354"
/clone_lib="NCI_CGAP_Brn20"
/tissue_type="oligodendroglioma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: brain; Vector: pAMP1; mRNA made from
oligodendroglioma tissue, cDNA made by oligo-dt priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 71 a 16 c 27 g 37 t
ORIGIN

Query Match 2.1%; Score 25; DB 10; Length 151;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||
Db 107 TTATTTCAAAAAAAAAAAAAAAAAA 131

RESULT 44

BE162370 162 bp mRNA EST 21-JUN-2000
LOCUS PM2-HT0451-090100-002-b03 HT0451 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BE162370
VERSION BE162370.1 GI:8625091
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 162)

Diagrams: Netto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-pw2-HT0451-090>)

100-002-b036t3-2000-01-09&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 150.

Location/Qualifiers
1. .162
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0451"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO.136,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 71 a 30 c 25 g 36 t

ORIGIN

Query Match 2.1%; Score 25; DB 10; Length 162;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||

Db 105 TTATTTCAAAAAAAAAAAAAAAAAA 129

RESULT 45
AW424467 174 bp mRNA EST 09-FEB-2000
LOCUS
DEFINITION
707016A03.y1 707 - Mixed adult tissues from walbot lab (SK) zea
mays cDNA, mRNA sequence.
ACCESSION
AW424467
VERSION
AW424467.1 GI:6952399
KEYWORDS
EST.
SOURCE
Zea mays.
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 174)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707016 row: A column: 03.
Location/Qualifiers
1. .174
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK)"
/tissue_type="tassel, kernel, silk, husk, root, leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: PGAD10; Site: 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."
BASE COUNT 85 a 28 c 19 g 41 t 1 others
ORIGIN

Query Match 2.1%; Score 25; DB 10; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1149 ttatttcaaaaaaaaaaaaaaaaaa 1173
|||||

Db 121 TTATTTCAAAAAAAAAAAAAAAAAA 145

RESULT 46
BE955607/c 181 bp mRNA EST 04-OCT-2000
LOCUS
DEFINITION
UI-M-CE1-bal-f-04-0-UI.s1 NIH_BMAP_Ret3.N Mus musculus cDNA clone
UI-M-CE1-bal-f-04-0-UI 3', mRNA sequence.
ACCESSION
BE955607
VERSION
BE955607.1 GI:10599321
KEYWORDS
EST.
SOURCE
house mouse.
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 181)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the retina tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 5-135, >B1-F#SINE/Alu 92-177, >B4#SINE/B4
Seq primer: M13 Forward

```

POLYA=Yes.
FEATURES
  source
    Location/Qualifiers
      1..181
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UI-M-CEI-bal-f-04-0-UI"
        /clone_lib="NIH-BMAP_Ret3_N"
        /dev_stage="6 weeks"
        /lab_host="PH10B (Life Technologies)"
        /note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH-BMAP_Ret3_N library is a normalized library derived
NIH-BMAP_Ret3. NIH-BMAP_Ret3 was made from mouse retina
tissue. For a detailed description of the library from
which this clone was derived, please visit our web site
at brainest.eng.uiowa.edu.
TAG_LTB=NIH-BMAP_Ret3_N
TAG_TISSUE=adult-retina
TAG_SEQ=GTCCGCGGCAC"
BASE COUNT 39 a 42 c 38 g 62 t
ORIGIN
Query Match 2.1%; Score 25; DB 11; Length 181;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1148 attatttcaaaaaaaaaaaaaa 1172
Db 25 ATTATTTCAAAAAAAAAAAAAAAAA 1

RESULT 47
AL377517 202 bp mRNA EST 03-AUG-2000
LOCUS MLEB32B08R1 MtBB Medicago truncatula cDNA clone MtBB32B08 T7, mRNA
DEFINITION sequence.
ACCESSION AL377517
VERSION AL377517.1 GI:9677269
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 202)
AUTHORS Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
,V. and Gamas,P.
TITLE Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
nodules
JOURNAL Unpublished (2000)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 2731326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Qualifiers
  1..202
    /organism="Medicago truncatula"
    /cultivar="Jemalong"
    /db_xref="taxon:3880"
    /clone="MtBB32B08"
    /clone_lib="MtBB"
    /tissue_type="symbiotic root nodules"
    /dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"

```

```

/note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2:
XhoI; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
cDNA was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exsist helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
BASE COUNT 57 a 34 c 25 g 86 t
ORIGIN
Query Match 2.1%; Score 25; DB 10; Length 202;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1149 ttatttcaaaaaaaaaaaaaa 1173
Db 175 TTATTTCAAAAAAAAAAAAAAAAA 199

RESULT 48
BE760641 218 bp mRNA EST 24-OCT-2000
LOCUS an.1998 Aspergillus niger, pYES2 (XhoI-EcoRI) Aspergillus niger
DEFINITION cDNA clone 1998 3', mRNA sequence.
ACCESSION BE760641
VERSION BE760641.1 GI:10183278
KEYWORDS EST.
SOURCE Aspergillus niger.
ORGANISM Aspergillus niger.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 218)
AUTHORS Tsang,A. and Storms,R.
TITLE Aspergillus niger Expressed Sequence Tags
JOURNAL Unpublished (2000)
COMMENT Contact: Tsang, A.
Dept. of Biology
Concordia University
1455 deMaisonneuve Blvd. West, Montreal, Quebec, CANADA, H3G 1M8
Tel: 514-848-3405
Fax: 514-848-4504
Email: tsang@vax2.concordia.ca
PCR PRIMERS
BACKWARD: GCGGTGAATGTAAAGCGTGACATAAC
Insert Length: 218 Std Error: 0.00
POLYA=Yes.
Location/Qualifiers
  1..218
    /organism="Aspergillus niger"
    /db_xref="taxon:5061"
    /clone="1998"
    /clone_lib="Aspergillus niger, pYES2 (XhoI-EcoRI)"
    /lab_host="E. coli"
    /note="Vector: pYES2; Site 1: XhoI; Site 2: EcoRI; cDNA
was synthesized with ZAP kit (Stratagene) using poly(A)+
RNA isolated from Aspergillus niger grown in both complete
and minimal media. Synthesis was primed with oligo(dT)
primer/XhoI-linker. EcoRI adaptors were later ligated to
polished ends. EcoRI-XhoI-digested cDNA was ligated with
EcoRI-XhoI-digested pYES2 (Invitrogen Corp). This vector
permits expression of our library in yeast."
BASE COUNT 61 a 52 c 30 g 71 t 4 others
ORIGIN

```


101	22	1.9	35100	5	PCT-US93-06251-19	Sequence 19, Appl	174	21	1.8	1660	1	US-08-626-994A-2	Sequence 2, Appl
102	22	1.9	56516	2	US-08-996-306-1	Sequence 1, Appl	175	21	1.8	1660	3	US-08-957-742-2	Sequence 2, Appl
103	22	1.9	56516	4	US-09-338-907-1	Sequence 1, Appl	176	21	1.8	1669	4	US-09-461-697-184	Sequence 184, App
104	22	1.9	56520	4	US-09-338-907-179	Sequence 179, App	177	21	1.8	1710	3	US-09-000-630C-1	Sequence 1, Appl
105	21	1.8	30	4	US-08-817-787-30	Sequence 30, Appl	178	21	1.8	1710	3	US-08-862-730C-1	Sequence 2, Appl
106	21	1.8	76	4	US-08-931-859E-139	Sequence 139, App	179	21	1.8	1720	3	US-08-705-771-2	Sequence 1, Appl
107	21	1.8	76	4	US-08-981-732-139	Sequence 139, App	180	21	1.8	1752	4	US-09-360-779-1	Sequence 1, Appl
108	21	1.8	383	4	US-09-020-956-82	Sequence 82, App	181	21	1.8	1849	2	US-08-912-227-1	Sequence 1, Appl
109	21	1.8	383	4	US-09-030-607-82	Sequence 82, App	182	21	1.8	1858	4	US-09-347-819-1	Sequence 1, Appl
110	21	1.8	384	4	US-09-030-607-183	Sequence 183, App	183	21	1.8	1869	3	US-08-966-318-4	Sequence 4, Appl
111	21	1.8	391	1	US-08-253-155A-24	Sequence 24, Appl	184	21	1.8	1969	4	US-09-216-619-4	Sequence 4, Appl
112	21	1.8	392	1	US-08-253-155A-60	Sequence 60, Appl	185	21	1.8	2070	1	US-08-486-342-1	Sequence 1, Appl
113	21	1.8	488	4	US-09-385-982-471	Sequence 471, App	186	21	1.8	2070	1	US-08-473-092-1	Sequence 1, Appl
114	21	1.8	575	1	US-08-554-659-11	Sequence 11, App	187	21	1.8	2076	1	US-08-614-801A-1	Sequence 1, Appl
115	21	1.8	599	4	US-09-328-111-147	Sequence 11, App	188	21	1.8	2076	1	US-08-066-371-1	Sequence 1, Appl
116	21	1.8	604	4	US-09-328-111-391	Sequence 147, App	189	21	1.8	2076	4	US-09-042-494-1	Sequence 1, Appl
117	21	1.8	684	1	US-08-226-264-27	Sequence 391, App	190	21	1.8	2076	5	PCT-US94-0566B-1	Sequence 1, Appl
118	21	1.8	723	2	US-08-618-911-1	Sequence 27, App	191	21	1.8	2114	1	US-07-803-622B-6	Sequence 1, Appl
119	21	1.8	737	1	US-08-602-262-1	Sequence 1, Appl	192	21	1.8	2207	4	US-08-956-322-3	Sequence 6, Appl
120	21	1.8	737	1	US-08-602-282-3	Sequence 3, Appl	193	21	1.8	2329	4	US-08-956-322-1	Sequence 3, Appl
121	21	1.8	737	3	US-09-004-716-1	Sequence 1, Appl	194	21	1.8	2336	2	US-08-389-564B-2	Sequence 2, Appl
122	21	1.8	742	1	US-09-004-716-3	Sequence 3, Appl	195	21	1.8	2336	2	US-08-466-047B-2	Sequence 2, Appl
123	21	1.8	780	2	US-07-847-010-12	Sequence 12, App	196	21	1.8	2567	3	US-08-993-260-4	Sequence 4, Appl
124	21	1.8	780	2	US-08-540-804-36	Sequence 36, App	197	21	1.8	2634	3	US-08-949-386-38	Sequence 38, App
125	21	1.8	820	4	US-08-590-399-36	Sequence 36, App	198	21	1.8	2671	1	US-08-450-562-26	Sequence 26, App
126	21	1.8	858	4	US-09-475-316A-28	Sequence 28, App	199	21	1.8	2671	5	US-08-408-519-1	Sequence 1, Appl
127	21	1.8	893	1	US-09-475-316A-14	Sequence 14, App	200	21	1.8	2712	3	PCT-US95-03559-1	Sequence 1, Appl
128	21	1.8	893	2	US-08-276-452A-66	Sequence 66, App	201	21	1.8	2712	3	US-08-450-562-38	Sequence 38, App
129	21	1.8	900	2	US-08-798-744-66	Sequence 66, App	202	21	1.8	2815	1	US-08-230-491A-1	Sequence 1, Appl
130	21	1.8	901	3	US-08-924-759-5	Sequence 5, Appl	203	21	1.8	2815	1	US-08-619-280A-1	Sequence 1, Appl
131	21	1.8	911	3	US-09-248-335-5	Sequence 5, Appl	204	21	1.8	2815	2	US-08-982-493-7	Sequence 7, Appl
132	21	1.8	911	3	US-09-248-335-33	Sequence 33, App	205	21	1.8	2818	4	US-08-628-655-1	Sequence 1, Appl
133	21	1.8	967	3	US-08-504-335-51	Sequence 51, App	206	21	1.8	2818	3	US-08-949-386-37	Sequence 37, App
134	21	1.8	974	2	US-08-540-459-13	Sequence 13, App	207	21	1.8	2970	3	US-08-450-562-37	Sequence 37, App
135	21	1.8	1046	1	US-08-361-467B-4	Sequence 4, Appl	208	21	1.8	3101	5	PCT-US93-06251-7	Sequence 7, Appl
136	21	1.8	1046	1	US-08-484-332C-4	Sequence 4, Appl	209	21	1.8	3471	5	US-08-868-786-1	Sequence 1, Appl
137	21	1.8	1063	1	US-08-325-562-1	Sequence 1, Appl	210	21	1.8	3471	5	US-08-832-883-48	Sequence 2, Appl
138	21	1.8	1063	1	US-08-437-795-1	Sequence 1, Appl	211	21	1.8	3865	1	US-08-832-883-48	Sequence 48, App
139	21	1.8	1074	2	US-08-975-316-54	Sequence 54, App	212	21	1.8	3865	2	US-08-832-887-48	Sequence 48, App
140	21	1.8	1075	2	US-08-975-316-55	Sequence 55, App	213	21	1.8	7567	4	US-08-378-313-22	Sequence 22, App
141	21	1.8	1163	4	US-09-160-588-1	Sequence 1, Appl	214	21	1.8	8743	3	US-09-081-320-1	Sequence 1, Appl
142	21	1.8	1233	3	US-08-853-839-1	Sequence 1, Appl	215	21	1.8	11492	4	US-08-991-840A-1	Sequence 1, Appl
143	21	1.8	1319	2	US-08-504-459-7	Sequence 7, Appl	216	21	1.8	4403765	4	US-09-103-840A-2	Sequence 2, Appl
144	21	1.8	1338	2	US-08-484-993B-7	Sequence 7, Appl	217	21	1.8	4411529	4	US-08-930-274-15	Sequence 15, Appl
145	21	1.8	1338	2	US-08-484-993B-7	Sequence 7, Appl	218	21	1.8	38	2	US-09-454-704A-7	Sequence 7, Appl
146	21	1.8	1338	2	US-08-484-993B-7	Sequence 7, Appl	219	21	1.8	38	4	US-08-510-032A-4	Sequence 4, Appl
147	21	1.8	1338	3	US-08-484-993B-7	Sequence 7, Appl	220	20	1.7	40	1	US-08-688-514-4	Sequence 4, Appl
148	21	1.8	1338	3	US-08-458-731-7	Sequence 7, Appl	221	20	1.7	40	3	US-09-306-290-15	Sequence 15, Appl
149	21	1.8	1338	3	US-08-149-223A-7	Sequence 7, Appl	222	20	1.7	40	4	US-09-306-290-26	Sequence 26, App
150	21	1.8	1365	1	US-08-114-072-1	Sequence 1, Appl	223	20	1.7	40	4	US-09-306-290-30	Sequence 30, App
151	21	1.8	1365	5	PCT-US94-09361-1	Sequence 1, Appl	224	20	1.7	43	4	US-09-306-290-37	Sequence 37, App
152	21	1.8	1428	4	US-09-118-442-5	Sequence 5, Appl	225	20	1.7	46	2	US-08-930-274-16	Sequence 16, App
153	21	1.8	1428	4	US-09-677-064-5	Sequence 5, Appl	226	20	1.7	115	2	US-08-930-274-11	Sequence 11, App
154	21	1.8	1433	1	US-07-968-371A-11	Sequence 11, App	227	20	1.7	123	2	US-08-153-051B-30	Sequence 30, App
155	21	1.8	1433	1	US-08-383-756-5	Sequence 5, App	228	20	1.7	142	1	US-08-060-952C-46	Sequence 46, App
156	21	1.8	1433	1	US-08-424-406-2	Sequence 2, App	229	20	1.7	142	3	US-08-151-477A-30	Sequence 30, App
157	21	1.8	1433	1	US-08-464-523B-8	Sequence 8, App	230	20	1.7	177	2	US-08-819-867-60	Sequence 60, App
158	21	1.8	1433	2	US-08-460-898-5	Sequence 5, App	231	20	1.7	232	2	US-08-849-701-6	Sequence 6, App
159	21	1.8	1442	1	US-08-468-763-18	Sequence 18, App	232	20	1.7	232	4	US-08-619-542B-28	Sequence 28, App
160	21	1.8	1442	2	US-08-393-996A-18	Sequence 18, App	233	20	1.7	260	3	US-09-191-136-29	Sequence 29, App
161	21	1.8	1502	4	US-09-206-903A-2	Sequence 2, App	234	20	1.7	288	1	US-08-688-988-19	Sequence 19, App
162	21	1.8	1502	4	US-09-206-903A-11	Sequence 11, App	235	20	1.7	288	1	US-08-849-701-7	Sequence 7, App
163	21	1.8	1502	4	US-09-202-122-2	Sequence 2, App	236	20	1.7	288	3	US-07-807-529A-38	Sequence 38, App
164	21	1.8	1502	4	US-09-202-122-11	Sequence 11, App	237	20	1.7	288	3	US-08-430-944D-102	Sequence 102, App
165	21	1.8	1502	4	US-09-206-935-2	Sequence 2, App	238	20	1.7	288	3	US-08-431-184-102	Sequence 102, App
166	21	1.8	1502	4	US-09-206-935-3	Sequence 3, App	239	20	1.7	310	3	US-08-702-344-10	Sequence 10, App
167	21	1.8	1502	4	US-09-206-936-2	Sequence 2, App	240	20	1.7	320	1	US-08-629-939-5	Sequence 5, App
168	21	1.8	1503	2	US-09-206-936-3	Sequence 3, App	241	20	1.7	320	1	US-08-759-873-5	Sequence 5, App
169	21	1.8	1558	1	US-08-715-325-1	Sequence 1, App	242	20	1.7	321	4	US-09-385-982-366	Sequence 366, App
170	21	1.8	1619	1	US-08-416-870C-9	Sequence 9, App	243	20	1.7				
171	21	1.8	1619	1	US-08-708-007A-1	Sequence 1, App	244	20	1.7				
172	21	1.8	1619	5	PCT-US94-04781-1	Sequence 1, App	245	20	1.7				
173	21	1.8	1639	2	US-08-737-524B-1	Sequence 1, App	246	20	1.7				

c 247	20	1.7	349	4	US-09-385-982-22	Sequence 22, Appl	320	20	1.7	783	2	US-08-457-364-34	Sequence 34, Appl
c 248	20	1.7	358	4	US-08-991-789A-168	Sequence 168, App	321	20	1.7	783	2	US-08-456-262-34	Sequence 34, Appl
c 249	20	1.7	370	1	US-08-330-535A-25	Sequence 25, Appl	322	20	1.7	783	2	US-08-456-240-34	Sequence 34, Appl
250	20	1.7	370	1	US-08-688-145-7	Sequence 7, Appl	323	20	1.7	783	2	US-08-455-736-34	Sequence 34, Appl
251	20	1.7	370	2	US-08-838-844-25	Sequence 25, Appl	324	20	1.7	783	2	US-08-971-217-34	Sequence 34, Appl
252	20	1.7	371	1	US-08-664-596B-25	Sequence 25, Appl	325	20	1.7	783	2	US-09-350-600-34	Sequence 34, Appl
253	20	1.7	371	2	US-08-739-775-3	Sequence 3, Appl	326	20	1.7	807	2	US-08-531-927B-9	Sequence 9, Appl
254	20	1.7	377	2	US-08-454-557C-37	Sequence 37, Appl	327	20	1.7	836	2	US-08-837-029-1	Sequence 1, Appl
255	20	1.7	377	2	US-08-340-426D-37	Sequence 37, Appl	328	20	1.7	836	2	US-08-967-364-4	Sequence 4, Appl
256	20	1.7	377	2	US-08-450-673C-37	Sequence 37, Appl	329	20	1.7	836	2	US-09-368-408-4	Sequence 4, Appl
257	20	1.7	377	5	PCT-US95-17111A-37	Sequence 37, Appl	330	20	1.7	836	2	US-08-831-570-2	Sequence 2, Appl
258	20	1.7	380	1	US-08-126-587C-5	Sequence 5, Appl	331	20	1.7	863	3	US-08-943-731-171	Sequence 171, App
259	20	1.7	390	1	US-08-661-168-7	Sequence 7, Appl	332	20	1.7	863	3	US-08-889-502-20	Sequence 20, Appl
c 260	20	1.7	423	3	US-08-943-731-131	Sequence 131, App	333	20	1.7	880	4	US-09-247-373B-39	Sequence 39, Appl
261	20	1.7	433	1	US-07-987-272A-13	Sequence 13, Appl	334	20	1.7	890	4	US-09-475-316A-3	Sequence 3, Appl
262	20	1.7	447	4	US-09-370-253-15	Sequence 15, Appl	335	20	1.7	903	5	PCT-US95-06406A-21	Sequence 21, Appl
263	20	1.7	469	1	US-08-468-347-23	Sequence 23, Appl	336	20	1.7	905	5	PCT-US96-07709-24	Sequence 24, Appl
264	20	1.7	469	1	US-08-226-284-25	Sequence 25, Appl	337	20	1.7	925	1	US-07-990-301A-3	Sequence 3, Appl
265	20	1.7	469	1	US-08-467-389-23	Sequence 23, Appl	338	20	1.7	932	3	US-08-906-616-88	Sequence 88, Appl
266	20	1.7	469	2	US-08-779-379-23	Sequence 23, Appl	339	20	1.7	932	3	US-08-817-795-88	Sequence 88, Appl
267	20	1.7	469	2	US-08-469-219-23	Sequence 23, Appl	340	20	1.7	932	3	US-08-639-075A-88	Sequence 88, Appl
268	20	1.7	469	4	US-09-228-152-23	Sequence 23, Appl	341	20	1.7	932	3	US-09-012-431-88	Sequence 31, Appl
269	20	1.7	522	1	US-08-289-247B-1	Sequence 1, Appl	342	20	1.7	932	4	US-09-032-215-31	Sequence 33, Appl
270	20	1.7	522	5	PCT-US95-09762-1	Sequence 1, Appl	343	20	1.7	932	4	US-09-012-692-88	Sequence 88, Appl
271	20	1.7	523	4	US-09-385-982-188	Sequence 188, App	344	20	1.7	932	4	US-08-906-613-88	Sequence 88, Appl
272	20	1.7	530	3	US-08-758-662-4	Sequence 4, Appl	345	20	1.7	932	5	PCT-US95-14442A-88	Sequence 37, Appl
273	20	1.7	567	1	US-08-661-168-6	Sequence 6, Appl	346	20	1.7	932	5	US-09-248-335-37	Sequence 3, Appl
274	20	1.7	571	2	US-08-803-899-1	Sequence 1, Appl	347	20	1.7	932	5	US-09-268-364-3	Sequence 1, Appl
c 275	20	1.7	581	4	US-09-020-956-103	Sequence 103, App	348	20	1.7	932	5	US-09-141-135-1	Sequence 1, Appl
c 276	20	1.7	581	4	US-09-030-607-103	Sequence 103, App	349	20	1.7	932	5	US-07-915-934-1	Sequence 1, Appl
c 277	20	1.7	582	4	US-09-328-111-569	Sequence 569, App	350	20	1.7	965	2	US-08-325-743-1	Sequence 24, Appl
c 278	20	1.7	583	4	US-09-030-607-203	Sequence 203, App	351	20	1.7	972	1	US-08-330-535A-24	Sequence 24, Appl
c 279	20	1.7	588	4	US-09-385-982-128	Sequence 128, App	352	20	1.7	972	1	US-08-874-460-1	Sequence 1, Appl
c 280	20	1.7	591	4	US-09-385-982-289	Sequence 289, App	353	20	1.7	1000	4	US-09-018-584A-33	Sequence 33, Appl
c 281	20	1.7	615	1	US-08-539-304A-1	Sequence 1, Appl	354	20	1.7	1000	4	US-09-018-584A-34	Sequence 34, Appl
c 282	20	1.7	615	4	US-09-385-982-528	Sequence 528, App	355	20	1.7	1000	4	US-09-357-251-19	Sequence 19, Appl
c 283	20	1.7	618	4	US-09-385-982-218	Sequence 218, App	356	20	1.7	1001	2	US-08-728-259A-10	Sequence 10, Appl
c 284	20	1.7	619	4	US-09-385-982-338	Sequence 338, App	357	20	1.7	1026	2	US-08-473-486-10	Sequence 10, Appl
c 285	20	1.7	623	4	US-09-385-982-512	Sequence 512, App	358	20	1.7	1026	2	US-08-713-000-6	Sequence 6, Appl
c 286	20	1.7	627	4	US-09-385-982-4	Sequence 4, Appl	359	20	1.7	1026	2	US-08-975-316-6	Sequence 6, Appl
c 287	20	1.7	640	4	US-09-385-982-2	Sequence 2, Appl	360	20	1.7	1026	2	US-09-211-710-6	Sequence 6, Appl
c 288	20	1.7	644	4	US-09-328-111-299	Sequence 299, App	361	20	1.7	1026	2	US-08-580-545B-5	Sequence 5, Appl
c 289	20	1.7	645	4	US-09-328-111-106	Sequence 106, App	362	20	1.7	1041	4	US-09-262-653A-5	Sequence 5, Appl
c 290	20	1.7	645	4	US-09-385-982-40	Sequence 40, Appl	363	20	1.7	1041	4	US-08-702-344-18	Sequence 18, Appl
c 291	20	1.7	646	4	US-09-385-982-314	Sequence 314, App	364	20	1.7	1041	4	US-09-222-734-3	Sequence 3, Appl
c 292	20	1.7	648	4	US-09-385-982-332	Sequence 332, App	365	20	1.7	1055	3	US-08-605-106-3	Sequence 3, Appl
c 293	20	1.7	650	4	US-09-328-111-179	Sequence 179, App	366	20	1.7	1055	3	US-08-934-959-1	Sequence 35, Appl
c 294	20	1.7	653	4	US-09-385-982-324	Sequence 324, App	367	20	1.7	1055	3	US-09-277-716-30	Sequence 30, Appl
c 295	20	1.7	659	4	US-09-003-574-20	Sequence 20, Appl	368	20	1.7	1055	3	US-08-036-555B-135	Sequence 135, App
c 296	20	1.7	689	4	US-09-003-570-20	Sequence 20, Appl	369	20	1.7	1055	3	US-08-469-569-135	Sequence 135, App
c 297	20	1.7	697	1	US-08-468-347-25	Sequence 25, Appl	370	20	1.7	1066	2	US-08-249-322A-135	Sequence 135, App
c 298	20	1.7	697	1	US-08-467-389-25	Sequence 25, Appl	371	20	1.7	1066	2	US-08-469-526A-135	Sequence 135, App
c 299	20	1.7	697	2	US-08-779-379-25	Sequence 25, Appl	372	20	1.7	1066	2	US-08-734-591A-135	Sequence 135, App
c 300	20	1.7	697	2	US-08-469-219-25	Sequence 25, Appl	373	20	1.7	1066	2	US-08-469-660-135	Sequence 135, App
c 301	20	1.7	697	4	US-09-228-152-25	Sequence 25, Appl	374	20	1.7	1066	2	US-08-341-018-5	Sequence 5, Appl
c 302	20	1.7	703	4	US-08-313-300-6	Sequence 6, Appl	375	20	1.7	1066	2	US-08-470-335-135	Sequence 135, App
c 303	20	1.7	729	1	US-08-447-010-1	Sequence 1, Appl	376	20	1.7	1066	2	US-08-735-021-135	Sequence 135, App
c 304	20	1.7	731	1	US-08-451-405A-2	Sequence 2, Appl	377	20	1.7	1066	2	US-08-734-664A-135	Sequence 135, App
c 305	20	1.7	739	1	US-08-363-010-3	Sequence 3, Appl	378	20	1.7	1066	2	US-08-470-339-135	Sequence 135, App
c 306	20	1.7	739	1	US-08-376-157B-3	Sequence 3, Appl	379	20	1.7	1066	2	PCT-US94-05083C-131	Sequence 131, App
c 307	20	1.7	775	1	US-09-004-731-9	Sequence 9, Appl	380	20	1.7	1066	2	PCT-US95-06846A-135	Sequence 135, App
c 308	20	1.7	775	4	US-09-004-731-11	Sequence 11, Appl	381	20	1.7	1066	2	US-08-469-667-15	Sequence 15, Appl
c 309	20	1.7	775	4	US-08-749-699-9	Sequence 9, Appl	382	20	1.7	1066	2	PCT-US95-07289-15	Sequence 15, Appl
c 310	20	1.7	775	4	US-08-749-699-11	Sequence 11, Appl	383	20	1.7	1066	2	PCT-US95-07289-15	Sequence 15, Appl
c 311	20	1.7	775	5	PCT-US96-00845-3	Sequence 3, Appl	384	20	1.7	1066	2	US-08-481-658B-39	Sequence 39, Appl
c 312	20	1.7	783	1	US-08-181-271A-34	Sequence 34, Appl	385	20	1.7	1066	2	US-08-477-504A-39	Sequence 39, Appl
c 313	20	1.7	783	1	US-08-449-315-34	Sequence 34, Appl	386	20	1.7	1066	2	US-08-486-756A-39	Sequence 39, Appl
c 314	20	1.7	783	1	US-08-444-803-34	Sequence 34, Appl	387	20	1.7	1066	2		
c 315	20	1.7	783	1	US-08-449-043-34	Sequence 34, Appl	388	20	1.7	1066	2		
c 316	20	1.7	783	1	US-08-456-265A-34	Sequence 34, Appl	389	20	1.7	1066	2		
c 317	20	1.7	783	1	US-08-455-416-34	Sequence 34, Appl	390	20	1.7	1066	2		
c 318	20	1.7	783	1	US-08-455-244-34	Sequence 34, Appl	391	20	1.7	1066	2		
c 319	20	1.7	783	1	US-08-454-876-34	Sequence 34, Appl	392	20	1.7	1066	2		

C 393	20	1.7	1174	2	US-08-485-862B-39	Sequence 39, Appl	466	20	1.7	1480	2	US-08-450-673C-38	Sequence 38, Appl
C 394	20	1.7	1174	3	US-08-787-739-39	Sequence 39, Appl	467	20	1.7	1480	5	PCT-US95-17111A-38	Sequence 38, Appl
C 395	20	1.7	1174	3	US-08-487-077A-39	Sequence 39, Appl	468	20	1.7	1485	1	US-08-471-601-23	Sequence 23, Appl
C 396	20	1.7	1174	3	US-08-485-863A-39	Sequence 39, Appl	469	20	1.7	1485	1	US-08-474-556-23	Sequence 23, Appl
C 397	20	1.7	1174	4	US-08-485-049D-39	Sequence 39, Appl	470	20	1.7	1485	1	US-08-479-382-23	Sequence 23, Appl
C 398	20	1.7	1174	4	US-09-178-115-39	Sequence 39, Appl	471	20	1.7	1485	1	US-08-470-354-23	Sequence 23, Appl
C 399	20	1.7	1174	4	US-09-177-776-39	Sequence 39, Appl	472	20	1.7	1485	1	US-08-479-383-23	Sequence 23, Appl
400	20	1.7	1189	4	US-09-147-779A-7	Sequence 7, Appl	473	20	1.7	1485	2	US-08-479-041-23	Sequence 23, Appl
401	20	1.7	1191	2	US-08-671-320-14	Sequence 14, Appl	474	20	1.7	1485	4	US-08-819-646-23	Sequence 23, Appl
402	20	1.7	1191	2	US-08-868-577-14	Sequence 14, Appl	475	20	1.7	1500	1	US-08-487-037-4	Sequence 4, Appl
403	20	1.7	1193	1	US-08-036-555B-134	Sequence 134, App	476	20	1.7	1501	4	US-09-196-520-1	Sequence 1, Appl
404	20	1.7	1193	1	US-08-469-569-134	Sequence 134, App	477	20	1.7	1505	3	US-08-909-965C-13	Sequence 1, Appl
405	20	1.7	1193	1	US-08-249-322A-134	Sequence 134, App	478	20	1.7	1536	3	US-08-993-359-29	Sequence 29, Appl
406	20	1.7	1193	1	US-08-469-526A-134	Sequence 134, App	479	20	1.7	1576	4	US-09-282-305-9	Sequence 9, Appl
407	20	1.7	1193	2	US-08-734-591A-134	Sequence 134, App	480	20	1.7	1581	4	US-09-313-300-1	Sequence 1, Appl
408	20	1.7	1193	2	US-08-469-660-134	Sequence 134, App	481	20	1.7	1587	3	US-09-108-020-11	Sequence 11, Appl
409	20	1.7	1193	3	US-08-341-018-3	Sequence 3, Appl	482	20	1.7	1596	4	US-09-146-950-17	Sequence 17, Appl
410	20	1.7	1193	3	US-08-470-335-134	Sequence 134, App	483	20	1.7	1602	4	US-08-530-950-3	Sequence 3, Appl
411	20	1.7	1193	4	US-08-735-021-134	Sequence 134, App	484	20	1.7	1602	3	US-08-888-429A-3	Sequence 3, Appl
412	20	1.7	1193	4	US-08-734-664A-134	Sequence 134, App	485	20	1.7	1602	4	US-09-149-879-3	Sequence 3, Appl
413	20	1.7	1193	4	US-08-470-339-134	Sequence 134, App	486	20	1.7	1616	4	US-09-370-253-11	Sequence 11, Appl
414	20	1.7	1193	5	PCT-US94-05083C-130	Sequence 130, App	487	20	1.7	1622	4	US-09-334-601-9	Sequence 9, Appl
415	20	1.7	1193	5	PCT-US95-06846A-134	Sequence 134, App	488	20	1.7	1624	2	US-08-852-807-10	Sequence 10, Appl
416	20	1.7	1196	3	US-07-959-509-4	Sequence 4, Appl	489	20	1.7	1624	4	US-08-430-225A-19	Sequence 19, Appl
417	20	1.7	1207	3	US-09-166-412-1	Sequence 1, Appl	490	20	1.7	1628	2	US-08-883-515-3	Sequence 3, Appl
418	20	1.7	1228	3	US-08-826-246-9	Sequence 9, Appl	491	20	1.7	1664	1	US-08-250-740-34	Sequence 34, Appl
419	20	1.7	1228	3	US-08-944-495-9	Sequence 9, Appl	492	20	1.7	1664	1	US-07-695-472B-3	Sequence 3, Appl
420	20	1.7	1228	3	US-09-126-640-5	Sequence 5, Appl	493	20	1.7	1689	4	US-09-061-702-3	Sequence 3, Appl
421	20	1.7	1228	4	US-08-925-588-9	Sequence 9, Appl	494	20	1.7	1706	1	US-07-906-871-11	Sequence 11, Appl
422	20	1.7	1242	2	US-08-909-965C-5	Sequence 5, Appl	495	20	1.7	1711	1	US-08-568-147B-1	Sequence 1, Appl
423	20	1.7	1260	4	US-08-943-731-169	Sequence 169, App	497	20	1.7	1712	3	US-09-058-389A-12	Sequence 12, Appl
424	20	1.7	1269	1	US-08-212-190A-1	Sequence 1, Appl	498	20	1.7	1724	4	US-08-509-024-1	Sequence 1, Appl
425	20	1.7	1269	2	US-08-900-321-1	Sequence 1, Appl	499	20	1.7	1724	5	PCT-US96-12374-1	Sequence 1, Appl
426	20	1.7	1269	5	PCT-US95-03610-1	Sequence 1, Appl	500	20	1.7	1724	4	US-09-360-197-13	Sequence 13, Appl
C 427	20	1.7	1275	3	US-08-725-532A-2	Sequence 2, Appl	501	20	1.7	1736	4	US-09-416-050A-7	Sequence 7, Appl
428	20	1.7	1275	3	US-08-909-965C-4	Sequence 4, Appl	502	20	1.7	1737	4	US-09-664-800-7	Sequence 7, Appl
429	20	1.7	1278	1	US-08-463-262A-1	Sequence 1, Appl	503	20	1.7	1737	4	US-09-665-309-7	Sequence 7, Appl
430	20	1.7	1299	1	US-08-463-989-1	Sequence 1, Appl	504	20	1.7	1737	4	US-09-661-569-7	Sequence 7, Appl
431	20	1.7	1299	4	US-09-003-574-1	Sequence 1, Appl	505	20	1.7	1741	1	US-08-565-655-5	Sequence 5, Appl
432	20	1.7	1299	4	US-09-003-570-1	Sequence 1, Appl	506	20	1.7	1759	1	US-08-726-525-5	Sequence 5, Appl
433	20	1.7	1313	3	US-09-035-648-22	Sequence 22, Appl	507	20	1.7	1759	2	US-08-487-942-5	Sequence 5, Appl
434	20	1.7	1313	4	US-09-001-951-22	Sequence 22, Appl	508	20	1.7	1759	2	US-08-726-036A-5	Sequence 5, Appl
435	20	1.7	1332	4	US-09-333-423-1	Sequence 44, Appl	509	20	1.7	1759	2	US-08-909-965C-10	Sequence 10, Appl
436	20	1.7	1334	2	US-08-481-658B-44	Sequence 44, Appl	510	20	1.7	1776	2	US-08-531-927B-1	Sequence 1, Appl
437	20	1.7	1334	2	US-08-477-504A-44	Sequence 44, Appl	511	20	1.7	1776	2	US-09-083-516-5	Sequence 5, Appl
438	20	1.7	1334	2	US-08-486-756A-44	Sequence 44, Appl	512	20	1.7	1776	4	US-09-041-886-12	Sequence 12, Appl
439	20	1.7	1334	2	US-08-485-862B-44	Sequence 44, Appl	513	20	1.7	1784	3	US-08-991-426-1	Sequence 1, Appl
440	20	1.7	1334	3	US-08-787-739-44	Sequence 44, Appl	514	20	1.7	1784	3	US-09-143-470-1	Sequence 1, Appl
441	20	1.7	1334	3	US-08-487-077A-44	Sequence 44, Appl	515	20	1.7	1817	3	US-08-564-86C-14	Sequence 14, Appl
442	20	1.7	1334	3	US-08-485-863A-44	Sequence 44, Appl	516	20	1.7	1821	4	US-09-056-105-23	Sequence 23, Appl
443	20	1.7	1334	4	US-08-485-863A-44	Sequence 44, Appl	517	20	1.7	1826	2	US-08-808-931-15	Sequence 15, Appl
444	20	1.7	1334	4	US-08-485-049D-44	Sequence 44, Appl	518	20	1.7	1826	3	US-08-808-323-15	Sequence 15, Appl
445	20	1.7	1334	4	US-09-178-115-44	Sequence 44, Appl	519	20	1.7	1826	3	US-09-050-603A-15	Sequence 15, Appl
446	20	1.7	1334	4	US-09-177-776-44	Sequence 44, Appl	520	20	1.7	1826	3	US-09-102-420B-15	Sequence 15, Appl
447	20	1.7	1342	2	US-08-909-965C-6	Sequence 6, Appl	521	20	1.7	1833	6	5166195-1	Patent No. 5166195
448	20	1.7	1347	4	US-09-140-804-1	Sequence 1, Appl	522	20	1.7	1837	2	US-08-909-965C-10	Sequence 10, Appl
449	20	1.7	1364	2	US-08-815-718-1	Sequence 1, Appl	523	20	1.7	1867	4	US-08-943-731-111	Sequence 111, App
450	20	1.7	1368	3	US-08-707-399B-1	Sequence 1, Appl	524	20	1.7	1875	2	US-08-683-743-3	Sequence 3, Appl
451	20	1.7	1377	4	US-08-810-572A-1	Sequence 1, Appl	525	20	1.7	1889	3	US-08-861-747-3	Sequence 3, Appl
452	20	1.7	1384	4	US-08-729-594A-33	Sequence 33, Appl	526	20	1.7	1896	1	US-08-253-503-1	Sequence 1, Appl
453	20	1.7	1392	1	US-08-957-351-1	Sequence 1, Appl	527	20	1.7	1896	1	US-08-796-883-1	Sequence 1, Appl
454	20	1.7	1393	1	US-08-052-205-2	Sequence 14, Appl	528	20	1.7	1896	2	US-08-611-273B-1	Sequence 1, Appl
455	20	1.7	1393	1	US-08-595-974-2	Sequence 63, Appl	529	20	1.7	1896	2	US-08-531-864-1	Sequence 1, Appl
456	20	1.7	1395	2	US-08-553-367A-1	Sequence 174, App	530	20	1.7	1896	2	US-08-373-636C-1	Sequence 1, Appl
457	20	1.7	1395	2	US-09-295-306-1	Sequence 3, Appl	531	20	1.7	1896	3	US-08-602-506A-1	Sequence 1, Appl
458	20	1.7	1410	5	PCT-US95-15428-14	Sequence 14, Appl	532	20	1.7	1896	4	US-09-266-294-1	Sequence 1, Appl
459	20	1.7	1459	4	US-08-821-994-63	Sequence 174, App	533	20	1.7	1896	4	US-09-179-281-1	Sequence 1, Appl
460	20	1.7	1459	4	US-09-020-956-174	Sequence 3, Appl	534	20	1.7	1896	4	US-09-056-105-25	Sequence 25, Appl
461	20	1.7	1459	4	US-09-030-607-174	Sequence 3, Appl	535	20	1.7	1901	5	PCT-US93-05000-32	Sequence 32, Appl
462	20	1.7	1470	1	US-08-052-205-3	Sequence 1, Appl	536	20	1.7	1901	5	US-08-826-611-1	Sequence 1, Appl
463	20	1.7	1470	1	US-08-595-974-3	Sequence 38, Appl	537	20	1.7	1901	5	US-09-146-950-1	Sequence 1, Appl
464	20	1.7	1476	1	US-08-872-302-1	Sequence 38, Appl	538	20	1.7	1929	4	US-08-627-907A-1	Sequence 1, Appl
465	20	1.7	1480	2	US-08-454-557C-38	Sequence 38, Appl	539	20	1.7	1933	3		

539	20	1.7	1952	1	US-08-333-358-1	Sequence 1, Appl	612	20	1.7	2729	1	US-07-938-782A-1	Sequence 1, Appl
540	20	1.7	1952	1	US-08-463-694-1	Sequence 1, Appl	613	20	1.7	2729	1	US-08-630-524-1	Sequence 1, Appl
541	20	1.7	1952	1	US-08-694-501-1	Sequence 1, Appl	614	20	1.7	2729	5	PCT-US93-08131-1	Sequence 1, Appl
542	20	1.7	1957	2	US-09-352-900-11	Sequence 11, Appl	615	20	1.7	2834	1	US-08-276-151-8	Sequence 8, Appl
543	20	1.7	1969	2	US-08-541-033A-7	Sequence 7, Appl	616	20	1.7	2886	2	US-08-687-080-55	Sequence 55, Appl
544	20	1.7	1969	2	US-08-828-451-7	Sequence 7, Appl	617	20	1.7	2923	1	US-08-480-449-1	Sequence 1, Appl
545	20	1.7	1977	2	US-08-574-959A-3	Sequence 3, Appl	618	20	1.7	2923	2	US-08-660-542-1	Sequence 5, Appl
546	20	1.7	1977	4	US-09-357-014-3	Sequence 3, Appl	619	20	1.7	2927	4	US-09-232-878-5	Sequence 5, Appl
547	20	1.7	2015	1	US-07-937-609-25	Sequence 25, Appl	620	20	1.7	2935	4	US-08-716-873-12	Sequence 12, Appl
548	20	1.7	2015	4	US-08-029-170-25	Sequence 25, Appl	621	20	1.7	2935	4	US-09-368-431-12	Sequence 12, Appl
549	20	1.7	2017	4	US-09-436-983-1	Sequence 1, Appl	622	20	1.7	3073	1	US-07-688-352C-31	Sequence 31, Appl
550	20	1.7	2022	2	US-08-464-517-32	Sequence 32, Appl	623	20	1.7	3073	2	US-08-474-379C-31	Sequence 31, Appl
551	20	1.7	2022	2	US-08-246-361A-32	Sequence 32, Appl	624	20	1.7	3073	3	US-09-146-249A-31	Sequence 31, Appl
552	20	1.7	2022	3	US-08-463-772-32	Sequence 32, Appl	625	20	1.7	3073	3	US-08-206-188B-31	Sequence 31, Appl
553	20	1.7	2026	1	US-08-503-133A-1	Sequence 1, Appl	626	20	1.7	3073	5	PCT-US91-0271A-30	Sequence 20, Appl
554	20	1.7	2026	2	US-08-576-775A-1	Sequence 1, Appl	627	20	1.7	3113	2	US-08-993-228-20	Sequence 20, Appl
555	20	1.7	2026	2	US-08-972-498-1	Sequence 1, Appl	628	20	1.7	3141	2	US-08-956-242-1	Sequence 1, Appl
556	20	1.7	2026	3	US-08-899-545-1	Sequence 1, Appl	629	20	1.7	3141	3	US-09-351-215-1	Sequence 1, Appl
557	20	1.7	2034	2	US-08-559-492-2	Sequence 2, Appl	630	20	1.7	3158	2	US-08-464-517-36	Sequence 36, Appl
558	20	1.7	2048	1	US-07-602-608-11	Sequence 11, Appl	631	20	1.7	3158	2	US-08-246-361A-36	Sequence 36, Appl
559	20	1.7	2048	1	US-08-261-578-11	Sequence 11, Appl	632	20	1.7	3158	3	US-08-463-772-36	Sequence 1, Appl
560	20	1.7	2059	1	US-08-256-130A-2	Sequence 2, Appl	633	20	1.7	3212	4	US-08-697-954-1	Sequence 5, Appl
561	20	1.7	2082	2	US-08-785-310A-2	Sequence 2, Appl	634	20	1.7	3238	4	US-08-123-934A-5	Sequence 5, Appl
562	20	1.7	2096	2	US-08-541-033A-19	Sequence 19, Appl	635	20	1.7	3238	5	PCT-US94-10080-5	Sequence 5, Appl
563	20	1.7	2096	2	US-08-828-451-19	Sequence 19, Appl	636	20	1.7	3350	1	US-08-247-946A-2	Sequence 2, Appl
564	20	1.7	2099	2	US-08-541-033A-3	Sequence 3, Appl	637	20	1.7	3350	3	US-09-110-116-2	Sequence 2, Appl
565	20	1.7	2099	4	US-08-828-451-3	Sequence 3, Appl	638	20	1.7	3350	5	PCT-US95-06420-2	Sequence 2, Appl
566	20	1.7	2099	4	US-08-938-669A-5	Sequence 5, Appl	639	20	1.7	3507	1	US-08-832-883-67	Sequence 67, Appl
567	20	1.7	2103	2	US-08-897-340-2	Sequence 2, Appl	640	20	1.7	3507	2	US-08-832-877-67	Sequence 67, Appl
568	20	1.7	2103	3	US-09-252-329-2	Sequence 2, Appl	641	20	1.7	3566	4	US-09-086-483A-1	Sequence 1, Appl
569	20	1.7	2119	2	US-08-381-691-17	Sequence 17, Appl	642	20	1.7	3585	1	US-08-362-670B-9	Sequence 9, Appl
570	20	1.7	2137	2	US-08-541-033A-18	Sequence 18, Appl	643	20	1.7	3585	3	US-08-333-576C-9	Sequence 9, Appl
571	20	1.7	2137	2	US-08-828-451-18	Sequence 18, Appl	644	20	1.7	3585	4	US-08-808-324-9	Sequence 9, Appl
572	20	1.7	2140	2	US-08-541-033A-1	Sequence 1, Appl	645	20	1.7	3585	5	PCT-US94-14030A-9	Sequence 4, Appl
573	20	1.7	2140	2	US-08-828-451-1	Sequence 1, Appl	646	20	1.7	3597	4	US-09-095-758-4	Sequence 4, Appl
574	20	1.7	2141	1	US-08-463-931-1	Sequence 1, Appl	647	20	1.7	3597	4	US-09-422-968-4	Sequence 8, Appl
575	20	1.7	2158	1	US-07-602-608-1	Sequence 1, Appl	648	20	1.7	3607	2	US-08-629-001A-8	Sequence 8, Appl
576	20	1.7	2158	1	US-08-261-578-1	Sequence 1, Appl	649	20	1.7	3607	4	US-08-642-274D-8	Sequence 8, Appl
577	20	1.7	2198	2	US-08-755-728-2	Sequence 2, Appl	650	20	1.7	3607	4	US-08-952-127-8	Sequence 8, Appl
578	20	1.7	2198	2	US-08-974-655-2	Sequence 2, Appl	651	20	1.7	3607	4	US-08-952-014C-8	Sequence 17, Appl
579	20	1.7	2198	4	US-09-283-011-2	Sequence 1, Appl	652	20	1.7	3692	2	US-08-588-983-17	Sequence 17, Appl
580	20	1.7	2226	3	US-08-951-260A-1	Sequence 3, Appl	653	20	1.7	3692	2	US-08-588-976-17	Sequence 5, Appl
581	20	1.7	2309	3	US-09-078-317-3	Sequence 3, Appl	654	20	1.7	3742	1	US-08-694-915-5	Sequence 3, Appl
582	20	1.7	2313	3	US-08-738-168B-14	Sequence 14, Appl	655	20	1.7	3771	1	US-08-185-432-3	Sequence 3, Appl
583	20	1.7	2335	4	US-09-387-574-9	Sequence 9, Appl	656	20	1.7	3771	1	US-09-112-096-28	Sequence 28, Appl
584	20	1.7	2343	3	US-09-031-392-1	Sequence 1, Appl	657	20	1.7	3848	4	US-08-185-432-3	Sequence 81, Appl
585	20	1.7	2343	3	US-09-299-549-1	Sequence 1, Appl	658	20	1.7	3867	4	US-09-347-114A-81	Sequence 1, Appl
586	20	1.7	2351	1	US-08-168-091A-1	Sequence 1, Appl	659	20	1.7	3885	1	US-08-688-145-1	Sequence 1, Appl
587	20	1.7	2362	1	US-08-265-087-1	Sequence 1, Appl	660	20	1.7	3946	3	US-09-083-351-1	Sequence 1, Appl
588	20	1.7	2362	1	US-08-621-493-1	Sequence 1, Appl	661	20	1.7	3946	4	US-09-083-352-1	Sequence 16, Appl
589	20	1.7	2362	2	US-08-965-688-1	Sequence 1, Appl	662	20	1.7	3952	2	US-08-381-691-16	Sequence 8, Appl
590	20	1.7	2362	2	US-08-965-688-1	Sequence 1, Appl	663	20	1.7	4032	1	US-08-126-587C-8	Sequence 17, Appl
591	20	1.7	2362	4	US-09-260-173-1	Sequence 2, Appl	664	20	1.7	4042	4	US-08-406-030A-17	Sequence 4, Appl
592	20	1.7	2381	5	PCT-US95-16980-2	Sequence 9, Appl	665	20	1.7	4131	1	US-08-484-565-4	Sequence 4, Appl
593	20	1.7	2381	1	US-08-726-160-9	Sequence 9, Appl	666	20	1.7	4131	1	US-08-480-751-4	Sequence 4, Appl
594	20	1.7	2381	5	PCT-US94-01782-9	Sequence 9, Appl	667	20	1.7	4131	2	US-08-943-986-4	Sequence 4, Appl
595	20	1.7	2384	1	US-08-021-608D-1	Sequence 1, Appl	668	20	1.7	4131	3	US-08-353-784-4	Sequence 4, Appl
596	20	1.7	2384	5	PCT-US94-01782-1	Sequence 1, Appl	669	20	1.7	4131	3	US-08-484-719B-4	Sequence 4, Appl
597	20	1.7	2413	4	US-09-518-046-1	Sequence 1, Appl	670	20	1.7	4195	1	US-08-200-016-1	Sequence 1, Appl
598	20	1.7	2416	4	US-09-261-416-1	Sequence 1, Appl	671	20	1.7	4326	2	US-08-852-807-12	Sequence 12, Appl
599	20	1.7	2420	5	PCT-US93-00227-1	Sequence 12, Appl	672	20	1.7	4326	3	US-09-187-049-1	Sequence 7, Appl
600	20	1.7	2447	4	US-08-387-707-12	Sequence 11, Appl	673	20	1.7	4337	3	US-08-845-998-7	Sequence 7, Appl
601	20	1.7	2448	2	US-08-687-080-111	Sequence 3, Appl	674	20	1.7	4524	3	US-09-206-537-7	Sequence 35, Appl
602	20	1.7	2544	4	US-09-518-046-3	Sequence 15, Appl	675	20	1.7	4524	4	US-09-430-854-7	Sequence 53, Appl
603	20	1.7	2555	2	US-08-960-022-15	Sequence 3, Appl	676	20	1.7	4524	4	US-09-103-663-35	Sequence 53, Appl
604	20	1.7	2555	2	US-08-326-286-3	Sequence 3, Appl	677	20	1.7	4550	4	US-08-832-883-53	Sequence 53, Appl
605	20	1.7	2587	2	US-08-326-286-3	Sequence 3, Appl	678	20	1.7	4586	2	US-08-832-877-53	Sequence 2, Appl
606	20	1.7	2589	6	5212286-1	Patent No. 5212286	679	20	1.7	4612	4	US-08-960-048-2	Sequence 1, Appl
607	20	1.7	2630	3	US-08-669-286-6	Sequence 6, Appl	680	20	1.7	4612	4	US-08-188-583-1	Sequence 2, Appl
608	20	1.7	2630	4	US-09-469-253-6	Sequence 6, Appl	681	20	1.7	4615	1	US-08-188-583-1	Sequence 1, Appl
609	20	1.7	2630	4	US-09-642-146-6	Sequence 6, Appl	682	20	1.7	4615	1	US-08-646-715-1	Sequence 1, Appl
610	20	1.7	2665	3	US-09-040-005-1	Sequence 1, Appl	683	20	1.7	4668	4	US-08-045-301-1	Sequence 1, Appl
611	20	1.7	2688	2	US-08-909-965C-1	Sequence 1, Appl	684	20	1.7	4671	4	US-08-462-437-27	Sequence 27, Appl

c 685	20	1.7	4741	1	US-07-695-472B-4	Sequence 4, Appli	c 758	20	1.7	10898	2	US-08-486-756A-5	Sequence 5, Appli
c 686	20	1.7	4742	1	US-08-250-740-35	Sequence 35, Appli	c 759	20	1.7	10898	2	US-08-485-862B-5	Sequence 5, Appli
c 687	20	1.7	4743	1	US-08-884-324-9	Sequence 9, Appli	c 760	20	1.7	10898	2	US-08-485-862B-5	Sequence 5, Appli
c 688	20	1.7	4843	3	US-08-986-485-1	Sequence 1, Appli	c 761	20	1.7	10898	3	US-08-787-739-5	Sequence 5, Appli
c 689	20	1.7	4978	1	US-08-220-603A-1	Sequence 1, Appli	c 762	20	1.7	10898	3	US-08-787-739-5	Sequence 5, Appli
c 690	20	1.7	5162	2	US-08-916-917-13	Sequence 13, Appli	c 763	20	1.7	10898	3	US-08-487-077A-5	Sequence 5, Appli
c 691	20	1.7	5162	3	US-09-225-170-13	Sequence 13, Appli	c 764	20	1.7	10898	3	US-08-487-077A-5	Sequence 5, Appli
c 692	20	1.7	5176	4	US-08-654-482-13	Sequence 13, Appli	c 765	20	1.7	10898	3	US-08-485-863A-5	Sequence 5, Appli
c 693	20	1.7	5232	4	US-08-972-927-13	Sequence 13, Appli	c 766	20	1.7	10898	3	US-08-485-863A-5	Sequence 5, Appli
c 694	20	1.7	5261	1	US-08-045-806-3	Sequence 1, Appli	c 767	20	1.7	10898	4	US-08-485-049D-5	Sequence 5, Appli
c 695	20	1.7	5261	3	US-08-368-051B-3	Sequence 3, Appli	c 768	20	1.7	10898	4	US-08-485-049D-5	Sequence 5, Appli
c 696	20	1.7	5375	3	US-08-757-223-7	Sequence 3, Appli	c 769	20	1.7	10898	4	US-09-178-115-5	Sequence 5, Appli
c 697	20	1.7	5499	1	US-07-695-564-4	Sequence 7, Appli	c 770	20	1.7	10898	4	US-09-178-115-5	Sequence 5, Appli
c 698	20	1.7	5499	1	US-08-241-387-4	Sequence 4, Appli	c 771	20	1.7	10898	4	US-09-177-776-5	Sequence 5, Appli
c 699	20	1.7	5590	4	US-07-050-159-129	Sequence 129, App	c 772	20	1.7	10898	4	US-09-177-776-5	Sequence 5, Appli
c 700	20	1.7	5629	1	US-07-695-564-2	Sequence 2, Appli	c 773	20	1.7	11298	4	US-07-869-933-31	Sequence 31, Appli
c 701	20	1.7	5629	1	US-08-241-387-2	Sequence 2, Appli	c 774	20	1.7	11298	4	US-08-201-879A-2	Sequence 2, Appli
c 702	20	1.7	5668	4	US-09-113-096-14	Sequence 14, Appli	c 775	20	1.7	11298	4	US-09-103-663-31	Sequence 31, Appli
c 703	20	1.7	5835	4	US-09-033-333-3	Sequence 3, Appli	c 776	20	1.7	11464	3	US-08-884-324-13	Sequence 13, Appli
c 704	20	1.7	5836	1	US-08-380-916-1	Sequence 1, Appli	c 777	20	1.7	11531	1	US-08-068-945A-1	Sequence 1, Appli
c 705	20	1.7	5836	3	US-08-721-690-1	Sequence 1, Appli	c 778	20	1.7	11531	1	US-08-442-806-1	Sequence 1, Appli
c 706	20	1.7	5836	3	US-08-891-581-1	Sequence 1, Appli	c 779	20	1.7	11613	1	US-08-484-044-10	Sequence 10, Appli
c 707	20	1.7	5836	4	US-09-033-333-2	Sequence 2, Appli	c 780	20	1.7	11811	4	US-09-078-294-7	Sequence 7, Appli
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c 709	20	1.7	6063	2	US-08-788-279-4	Sequence 4, Appli	c 782	20	1.7	13158	2	US-08-687-080-105	Sequence 105, App
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c 846	19	1.6	30	1	US-08-483-553-41	Sequence 41, Appl	c 919	19	1.6	70	3	US-08-295-802-43	Sequence 43, Appl
c 847	19	1.6	30	1	US-08-487-002-41	Sequence 41, Appl	c 920	19	1.6	70	4	US-08-488-237A-43	Sequence 43, Appl
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c 869	19	1.6	42	3	US-08-486-414-11	Sequence 11, Appl	c 942	19	1.6	93	3	US-08-651-472-40	Sequence 40, Appl
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977 19 1.6 123 4 US-09-244-796-1
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ALIGNMENTS

RESULT 1
US-08-924-747-1
; Sequence 1, Application US/08924747
; Patent No. 6063570
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,747
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: SE1.27B04

US-08-924-747-1

Query Match 2.0%; Score 24; DB 3; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 TATTTCACAAAAA 886

RESULT 2

US-09-247-373B-1
; Sequence 1, Application US/09247373B
; Patent No. 6168954
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
; FILE REFERENCE: CL-1108-A
; CURRENT APPLICATION NUMBER: US/09/247,373B
; CURRENT FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 08/924,747
; PRIOR FILING DATE: 1997-09-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 886
; TYPE: DNA
; ORGANISM: SOYBEAN
US-09-247-373B-1

Query Match 2.0%; Score 24; DB 4; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 863 tatttcaaaaaaaaaaaaaa 886

RESULT 3

US-09-296-715-1
; Sequence 1, Application US/09296715
; Patent No. 6171839
; GENERAL INFORMATION:
; APPLICANT: MCGONIGLE, BRIAN
; APPLICANT: O'KEEFE, DANIEL
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
; TITLE OF INVENTION: ENZYMES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/296,715
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1108

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 886 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: SEI.27B04
; US-09-296-715-1

Query Match 2.0%; Score 24; DB 4; Length 886;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

Db 863 TATTTCACAAAAA 886

RESULT 4

US-09-323-427-6
; Sequence 6, Application US/09323427
; Patent No. 6248329
; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Morales, Tony H.
; TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
; TITLE OF INVENTION: Molecules, and Uses Thereof
; FILE REFERENCE: HW-8
; CURRENT APPLICATION NUMBER: US/09/323,427
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 60/087,435
; EARLIER FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1372
; TYPE: DNA
; ORGANISM: Dirofilaria immitis
; US-09-323-427-6

Query Match 2.0%; Score 24; DB 4; Length 1372;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

Db 1341 tatttcaaaaaaaaaaaaaaa 1364

RESULT 5

US-09-323-427-7/c
; Sequence 7, Application US/09323427
; Patent No. 6248329
; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramaswamy
; APPLICANT: Morales, Tony H.
; TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
; TITLE OF INVENTION: Molecules, and Uses Thereof
; FILE REFERENCE: HW-8
; CURRENT APPLICATION NUMBER: US/09/323,427
; CURRENT FILING DATE: 1999-06-01
; EARLIER APPLICATION NUMBER: 60/087,435
; EARLIER FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1372
; TYPE: DNA
; ORGANISM: Dirofilaria immitis
; US-09-323-427-7

Query Match 2.0%; Score 24; DB 4; Length 1372;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1173
|||||

Db 32 TATTTCACAAAAA 9

RESULT 6

US-08-175-158A-1
; Sequence 1, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MacGILLIVRAY, Ross T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175.158A
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..2124
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 88..2124
; US-08-175-158A-1

Query Match 2.0%; Score 24; DB 2; Length 2327;
Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 2293 TATTTCACAAAAAAAAAAAAA 2316

RESULT 7

US-08-415-593-42
; Sequence 42, Application US/08415593
; Patent No. 5912140
; Patent No. 5912140 5776726
; GENERAL INFORMATION:
; APPLICANT: Whoriskey, Susan K.
; APPLICANT: Quinn, Cheryl L.
; APPLICANT: Tao, Nijun
; APPLICANT: Politis-Virk, Karen I.
; APPLICANT: Schimmel, Paul R.
; TITLE OF INVENTION: Recombinant Pneumocystis Aminoacyl tRNA
; TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,593
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CPI94-09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-862-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2934
US-08-415-593-42

Query Match 2.0%; Score 24; DB 2; Length 2993;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaa 1173
|||||
Db 2963 TATTTCACAAAAAAAAAAAAA 2986

RESULT 8

US-08-996-306-10/c
; Sequence 10, Application US/08996306
; Patent No. 5945522
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya

; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,306
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: GENSET.018A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PGRT32
; LOCATION: complement 5198..5221
; OTHER INFORMATION: Location relative to seqID3
US-08-996-306-10

Query Match 2.0%; Score 23; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaa 1173
|||||
Db 24 ATTTCACAAAAAAAAAAAAA 2

RESULT 9

US-09-338-907-10/c
; Sequence 10, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18C1P
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm

; SEQ ID NO 10
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..24
; OTHER INFORMATION: primer oligonucleotide PGRT32
; US-09-338-907-10

Query Match 2.0%; Score 23; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 24 ATTTCAAAAAAAAAAAAAAAAA 2

RESULT 10
US-08-741-881-3/c
; Sequence 3, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-741-881-3

Query Match 2.0%; Score 23; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 11
US-08-739-158-3/c
; Sequence 3, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-739-158-3

Query Match 2.0%; Score 23; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 12
US-08-739-167-3/c
; Sequence 3, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-3

Query Match 2.0%; Score 23; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||
DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 13
US-08-404-796-3/c
Sequence 3, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-3

Query Match 2.0%; Score 23; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||
DB 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 14
US-08-931-869-3/c
Sequence 3, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-3

Query Match 2.0%; Score 23; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaaa 1173
|||||

Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 15

US-08-741-881-21/c
; Sequence 21, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.42306 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-21

Query Match 2.0%; Score 23; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173
Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 16

US-08-739-158-21/c
; Sequence 21, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle

; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-21

Query Match 2.0%; Score 23; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaaaaaa 1173
Db 41 ATTTCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 17

US-08-739-167-21/c
; Sequence 21, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-167-21

Query Match 2.0%; Score 23; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 18
US-08-404-796-21/c
; Sequence 21, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-404-796-21

Query Match 2.0%; Score 23; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 19
US-08-931-869-21/c
; Sequence 21, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-21

Query Match 2.0%; Score 23; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 41 ATTTCAAAAAAAAAAAAAAAAA 19

RESULT 20
US-08-826-246-7
; Sequence 7, Application US/08826246
; Patent No. 6048709
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

```
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...546
OTHER INFORMATION:
US-08-826-246-7

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 TATTCAAAAAAAAAAAAAA 888

RESULT 21
US-08-944-495-7
Sequence 7, Application US/08944495
Patent No. 6087477
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495
```

```
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...546
OTHER INFORMATION:
US-08-944-495-7

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 TATTCAAAAAAAAAAAAAA 888

RESULT 22
US-09-126-640-4
Sequence 4, Application US/091266404
Patent No. 6099823
GENERAL INFORMATION:
APPLICANT: Falb, Dean A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FILE REFERENCE: 7853-126
CURRENT APPLICATION NUMBER: US/09/126,6404
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 08/870,434
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
EARLIER APPLICATION NUMBER: 60/011,787
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1036
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1036)
OTHER INFORMATION: n = A,T,C or G
US-09-126-640-4

Query Match 2.0%; Score 23; DB 3; Length 1036;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1150 tatttcaaaaaaaaaaaaaa 1172
|||||
DB 866 tatttcaaaaaaaaaaaaaa 888
```

RESULT 23

US-08-925-588-7
; Sequence 7, Application US/08925588
; Patent No. 6221628

GENERAL INFORMATION:

APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF
CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/925,588

FILING DATE: 08-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/799,910

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-067-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)7909090

TELEFAX: (212)8699741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1036 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1..546

OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-08-925-588-7

Query Match 2.0%; Score 23; DB 4; Length 1036;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1150 tatttcaaaaaaaaaaaaaaa 1172

| | | | |

Db 866 TATTTCAAAAAAAAAAAAAA 888

RESULT 24

US-09-187-124-1

; Sequence 1, Application US/09187124A

; Patent No. 6255563

; GENERAL INFORMATION:

APPLICANT: Emmermann, Michael

APPLICANT: Kossmann, Jeos

TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES

TITLE OF INVENTION: FROM POTATO

FILE REFERENCE: GFB8

; CURRENT APPLICATION NUMBER: US/09/187,124A
; CURRENT FILING DATE: 1998-11-05

; EARLIER APPLICATION NUMBER: PCT/EP97/02292

; EARLIER FILING DATE: 1997-05-06

; EARLIER APPLICATION NUMBER: DE 196 18 125.9

; EARLIER FILING DATE: 1996-05-06

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2133

; TYPE: DNA

; ORGANISM: Solanum tuberosum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(1819)

; OTHER INFORMATION: Clone: Iso5

US-09-187-124-1

Query Match 2.0%; Score 23; DB 4; Length 2133;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaa 1173

| | | | |

Db 2054 atttcaaaaaaaaaaaaaaa 2076

RESULT 25

US-08-264-101-1

; Sequence 1, Application US/08264101

; Patent No. 5693496

; GENERAL INFORMATION:

APPLICANT: ALVES, KENNETH

APPLICANT: GUPTA, SUNIL K.

APPLICANT: HOLLIS, GREGORY F.

TITLE OF INVENTION: CONTRACEPTIVE VACCINE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: MARY A. APPOLLINA

STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/264,101

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: APPOLLINA, MARY A.

REGISTRATION NUMBER: 34,087

REFERENCE/DOCKET NUMBER: 19244

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3462

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2373 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-264-101-1

Query Match 2.0%; Score 23; DB 1; Length 2373;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 2309 ATTTCAAAAAAAAAAAAAAAA 2331

RESULT 26

US-08-765-243-1
; Sequence 1, Application US/08765243
; Patent No. 5935578
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08765,243
; FILING DATE:

CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-765-243-1

Query Match 2.0%; Score 23; DB 2; Length 2373;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 2309 ATTTCAAAAAAAAAAAAAAAA 2331

RESULT 27

PCT-US95-07295-1
; Sequence 1, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ

COUNTRY: USA
; ZIP: 07065
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APPOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-07295-1

Query Match 2.0%; Score 23; DB 5; Length 2373;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||
Db 2309 ATTTCAAAAAAAAAAAAAAAA 2331

RESULT 28

US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-972-218-2

Query Match 2.0%; Score 23; DB 4; Length 9521;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

Db 7123 ATTTCAAAAAAAAAAAAAAAAA 7145

RESULT 29
US-08-972-218-1
; Sequence 1, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Orberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13905 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-1

Query Match 2.0%; Score 23; DB 4; Length 13905;
Best Local Similarity 100.0%; Pred. No. 0.95;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

Db 11666 ATTTCAAAAAAAAAAAAAAAAA 11988

RESULT 30
US-08-741-881-1
; Sequence 1, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-1

Query Match 2.0%; Score 23; DB 1; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 31
US-08-739-158-1
; Sequence 1, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SEED and BERRY LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/739,158
;; FILING DATE: 30-OCT-1996
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16656 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-739-158-1

Query Match 2.0%; Score 23; DB 1; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1151 attcagaaaaaa 1173
||||| 11718

Db 11696 attcagaaaaaa 11718

RESULT 32
US-08-739-167-1
; Sequence 1, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,167
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.

;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16656 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-739-167-1

Query Match 2.0%; Score 23; DB 2; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1151 attcagaaaaaa 1173
||||| 11718

Db 11696 attcagaaaaaa 11718

RESULT 33
US-08-404-796-1
; Sequence 1, Application US/08404796
; Patent No. 6015686
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,796
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16656 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-404-796-1

Query Match 2.0%; Score 23; DB 3; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 34

US-08-931-869-1
; Sequence 1, Application US/08931869
; Patent No. 6015694
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,869
; FILING DATE: 16-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/404,796
; FILING DATE: 15-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16656 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-931-869-1

Query Match 2.0%; Score 23; DB 3; Length 16656;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 11696 ATTTCAAAAAAAAAAAAAAAAA 11718

RESULT 35

US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155

; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 2.0%; Score 23; DB 3; Length 152331;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaa 1173
|||||
Db 61197 ATTTCAAAAAAAAAAAAAAAAA 61175

RESULT 36

US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:

NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 37

US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-21

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 38

US-08-724-394A-22

; Sequence 22, Application US/08724394A

; Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-22

Query Match 2.0%; Score 23; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1151 atttcaaaaaaaaaaaaaaaaa 1173
|||||

DB 141094 ATTTCAAAAAAAAAAAAAAAAA 141116

RESULT 39

US-09-306-290-21/c

; Sequence 21, Application US/09306290

; Patent No. 6221635

GENERAL INFORMATION:

APPLICANT: Rovera, Giovanni

APPLICANT: Mukhopadhyay, Sunil

TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE

TITLE OF INVENTION: (SPADT) USING MULTARRAYS

; FILE REFERENCE: 09924-10
; CURRENT APPLICATION NUMBER: US/09/306,290
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer p41
; OTHER INFORMATION: FH92
US-09-306-290-21

Query Match 1.9%; Score 22; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.4; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1152 ttccaaaaa 1173
Db 25 TTTCAAAAAA 4

RESULT 40
US-08-991-840A-13/c
; Sequence 13, Application US/08991840A
; Patent No. 6261570
; GENERAL INFORMATION:
; APPLICANT: Michael D. Parker
; APPLICANT: Jonathan F. Smith
; APPLICANT: Bruce Crise
; APPLICANT: Mark Steve Oberste
; APPLICANT: Shannon Schmura
; TITLE OF INVENTION: Live Attenuated Virus Vaccines for Eastern Equine Encephalitis
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: USA MRC - MRC-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,840A
; FILING DATE: December 16, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Provisional Application 60/047162,
; FILING DATE: May 20, 1997
; APPLICATION NUMBER: Provisional Application 60/053,652
; FILING DATE: July 24, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: 003/058/SAP RIID 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-5034
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
US-08-991-840A-13

Query Match 1.9%; Score 22; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.4; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1151 attcaaaaa 1172
Db 34 ATTCAAAAAA 13

RESULT 41
US-08-482-182-70
; Sequence 70, Application US/08482182
; Patent No. 5861273
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, DESMOND
; APPLICANT: OLSON, PAMELA S.
; TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
; TITLE OF INVENTION: GENES IN BACTERIAL CELLS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,182
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 22095-20281.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-182-70

Query Match 1.9%; Score 22; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 584 gcaccaccaccaccacgac 605
Db 31 GCACCACCACCACCACGAC 52

RESULT 42
US-08-747-121-2
; Sequence 2, Application US/08747121
; Patent No. 5874290
; GENERAL INFORMATION:
; APPLICANT: Murphy, Gerald
; APPLICANT: Boynton, Alton
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID
; TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
; TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 20

;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/747,121
;; FILING DATE: 08-NOV-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Baldwin, Geraldine F
;; REGISTRATION NUMBER: 31,232
;; REFERENCE/DOCKET NUMBER: 8511-008
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)7909090
;; TELEFAX: (212)8698864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 144 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-747-121-2

Query Match 1.9%; Score 22; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1152 ttccaaaaaiaaaaaaaaaa 1173
|||||

Db 122 TTTCAAAAAAAAAAAAAAAAAA 143

RESULT 43
US-09-385-982-387/c
; Sequence 387, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 387
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-385-982-387

Query Match 1.9%; Score 22; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1152 ttccaaaaaiaaaaaaaaaa 1173
|||||

Db 35 TTTCAAAAAAAAAAAAAAAAAA 14

RESULT 44
US-09-385-982-508
; Sequence 508, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 508
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(336)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-508

Query Match 1.9%; Score 22; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaiaaaaaaaaaa 1173
|||||

Db 309 ttccaaaaaiaaaaaaaaaa 330

RESULT 45
US-09-385-982-203/c
; Sequence 203, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(577)
; OTHER INFORMATION: n = A,T,C or G

```
us-09-385-982-203

Query Match          1.9%; Score 22; DB 4; Length 577;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 ttcaaaaaaaaaaaaaaaaa 1173
   |||||
Db 55 TTTCAAAAAAAAAAAAAAAAAA 34

RESULT 46
US-08-557-309B-22
; Sequence 22, Application US/08557309B
; Patent No. 5916572
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,309B
; FILING DATE: 14-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-557-309B-22

Query Match          1.9%; Score 22; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 ttcaaaaaaaaaaaaaaaaa 1173
   |||||
Db 541 TTTCAAAAAAAAAAAAAAAAAA 562

RESULT 47
US-08-834-306-22
; Sequence 22, Application US/08834306
; Patent No. 6054135
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.

us-09-385-982-203

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,306
FILING DATE: 15-APR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.422C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-834-306-22

Query Match          1.9%; Score 22; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 ttcaaaaaaaaaaaaaaaaa 1173
   |||||
Db 541 TTTCAAAAAAAAAAAAAAAAAA 562

RESULT 48
US-08-993-674A-22
; Sequence 22, Application US/08993674A
; Patent No. 6228372
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,674A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```


; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-993-674A-22

Query Match 1.9%; Score 22; DB 4; Length 581;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaa 1173
Db 541 TTTCAAAAAA 562

RESULT 49

US-09-091-590A-2
; Sequence 2, Application US/09091590A
; Patent No. 6242574
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Klaus
; APPLICANT: Kroll Kristensen, Anne
; APPLICANT: Brunstedt, Janne
; TITLE OF INVENTION: Anti-Microbial Proteins
; FILE REFERENCE: S-137-1101/NA/A/SGS/PCT
; CURRENT APPLICATION NUMBER: US/09/091,590A
; CURRENT FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: PCT/JEP96/05765
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: GB 9526238.2
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Beta vulgaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)..(374)
US-09-091-590A-2

Query Match 1.9%; Score 22; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaa 1173
Db 566 ttccaaaaaa 587

RESULT 50

US-09-385-982-265/c
; Sequence 265, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111

; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 265
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(592)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-265

Query Match 1.9%; Score 22; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1152 ttccaaaaaa 1173
Db 36 TTTCAAAAAA 15

Search completed: December 27, 2001, 15:00:45
Job time: 697 sec

